

[illegible]

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<210> 5
<211> 255
<212> DNA
<213> Escherichia coli
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<210> 6
<211> 395
<212> DNA
<213> Escherichia coli
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<210> 7
<211> 280
<212> DNA
<213> Escherichia coli
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<210> 8
<211> 363
<212> DNA
<213> Escherichia coli
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gcactggagg caaccgcatt aatcaacgtg aaatacgact aataacaagc aagacgagca 180
 agtggctaata aataaaaaat aacaagggtg ctgcatttcc ccctcatgat gaggggggctt 240
 tttttagcga tgataaaaaa tctcaccgtc gtaggcttta atgattttac cgtcgggtgc 300
 gctgatcaac acgtacgcgc caccatata ggtccagtgc gtcccggcat caggcgcggg 360
 cag 363

<210> 9
 <211> 295
 <212> DNA
 <213> Escherichia coli

<400> 9
 ttacagatac aacggtttca attccgataa cagccagtta ctacgtctac gatacaaaaca 60
 aagttaaatc tggcgactg gaggcaaccg cattaatcaa cgtgaaatac gactaataac 120
 aagcaagacg agcaagtggc taataataaa aaataacaag gtgtctgcat tccccctca 180
 tgatgagggg gcttttttta gcgatgataa aaaatctcac cgtcgtaggc tttaatgatt 240
 ttaccgtcgg tgtcgtgat caacacgtac gcgccacca tatagggtcca gtgcg 295

<210> 10
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 10
 acgactaata acaagcaaga cgagcaagtg gctaataata aaaaataaca aggtgtctgc 60
 atttccccct catgatgagg gggctttttt tagcgatgat aaaaaatctc accgtcgtag 120
 gctttaatga ttttaccgtc ggtgtcgtg atcaacacgt a 161

<210> 11
 <211> 290
 <212> DNA
 <213> Escherichia coli

<400> 11
 tgcggcgaag tcaaaactta cagatacaac ggtttcaatt ccgataacag ccagttacta 60
 cgtctacgat acaaacaaag ttaaatctgg cgactggag gcaaccgcat taatcaacgt 120
 gaaatacgac taataacaag caagacgagc aagtggctaa taataaaaaa taacaagggtg 180
 tctgcatttc cccctcatga tgagggggct ttttttagcg atgataaaaa atctcaccgt 240
 cgtaggcttt aatgatttta ccgtcgggtg cgctgatcaa cacgtacgcg 290

<210> 12
 <211> 137
 <212> DNA
 <213> Escherichia coli

<400> 12
 ctggttttag cttttgcttc gtaaacacgt aataaaacgt cctcacacaa tatgaggacg 60
 ccgaatttta gggcgatgcc gaaaagggtg caagaaatat acaacgatcc cgccatcacc 120
 aggccatctg gctgggg 137

<210> 13
 <211> 275
 <212> DNA
 <213> Escherichia coli

<400> 13
 cgtcatgtac gtgcagtttg gtcgtacgct tgatgaattt accgtagatc ggggtgtttca 60

caaaacgttc gatagcaaca acaatggatt tctccatttt gtcgctaaca acgcgacctt 120
gcagagtacg gattttatcg gtcattacgc acccgcttc tcgttcagta aagtcttaac 180
gcgtgcgaca tcgcgacgca cttgcttcaa cagggtgagac tggttcagct ggccacttgc 240
agcctgcata cgcaggttga actgctcacg cagca 275

<210> 14
<211> 239
<212> DNA
<213> Escherichia coli

<400> 14
tgtcggtaaa caatgacaat ttgagacaga gtgaaaggtc agatttgagg agtaatgcac 60
ataatgggta tttaaataaa ccacatgaat cattaatggg ttattcatta tttttgtgat 120
ttactcacia tgtatcaggg aaatataact taccgggaga tgtaatatgt ttaatttttc 180
aaatcgaaat ttaaaatatt gtgccggagg catctctggc acattgggca attacggca 239

<210> 15
<211> 114
<212> DNA
<213> Escherichia coli

<400> 15
cgatgttctg aatctgctcg cgcattctgt caatcaacac tttcagctcg atggcggagt 60
ttgtcacttc ggcattgata gacttcgacg caagagtgtt cgactcgcgg ttga 114

<210> 16
<211> 290
<212> DNA
<213> Escherichia coli

<400> 16
acgggaagta attgtaactt agtttgtaaa ggtcatatgc ttgttgatat ttcttttttg 60
gctgacatac tgatgcaaaa tcttttagat actcatgatt ttcgaacgca taaatgcaca 120
agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggtag tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattattg 290

<210> 17
<211> 444
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

<400> 17
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gctgacatac tgatgcaaaa tcttttagat actcatgatt ttcgaacgca taaatgcaca 120
agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggtag tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattantg aatatttcaa 300
ttgtttctgt gtcataata ttctctgng atgtgntctg ngatgccnaa cnattatttg 360
antgactcat ngnnatnttt atatnnatcc nntnntaant natnantntn aagccngcnt 420
tgcttatggg ntantntnat ttat 444

<210> 18
<211> 250
<212> DNA
<213> Escherichia coli

<400> 18
cgctggaaaa aacctaataat attcatctta ttccccctac gagaacccta tttggctcgt 60
ttcaagccgt atttttattt tgctgcaaatt tgtactgccg atgttctgta atcagattgt 120
tagatcatct gctacagagt gtgtgaaaat ttaattcgta tcgcaaatta aacgcgtgtc 180
ttttgtgagt tttgtcacca aatatcgta ttatcactcc cttttactgg ctaaaccaga 240
aaacttattt 250

<210> 19
<211> 237
<212> DNA
<213> Escherichia coli

<400> 19
gtattacaac aagaatacag tgctaaaaaa agaatgtacc tgaagatagt cttcattttt 60
actccaatgt ttctttattg ttatggtttg cgctgttttt gtttggtatt cgtagtaaat 120
atccactaac acatggctca taagtgtacc agatgtaaca ctcaatgcag gatcgatttt 180
ttgcattcgg gtgctaaatt tccaggatga accattcatg tcatccgaca ttactgg 237

<210> 20
<211> 237
<212> DNA
<213> Escherichia coli

<400> 20
catcatcaca gcggcagcca tgtacagcag atccatattc aggtttttcca tgacagtctc 60
cagtttgttt cagttaaaac gtagtagtgt tggtaaatta atgttcttca gacgccatcg 120
acagatagac gatcgtcaga accatgaaga tgaaggcttg cagcgtaatg atcaggatgt 180
ggaaaatggc ccacggcaca ttcaggatcc actgtgacca ccacggcaac agaccag 237

<210> 21
<211> 139
<212> DNA
<213> Escherichia coli

<400> 21
cccgcgacgt tatccgcgtg taggcatcgt catgacgtaa acggcgatcg gcggtataac 60
ggttgatcat cgaatccatg ttgccagcag taacaccgaa aaacagattc ggtttaccga 120
gacgcataaa gtcgtcttt 139

<210> 22
<211> 211
<212> DNA
<213> Escherichia coli

<400> 22
ggagagcgaa gggctatccg gccagggtga aattatcgcc gcgaacgcac aatttgatat 60
cgacgagtaa agtactcaaa cggcgcgctc cacacatgca ccagtcgggt gaacgggaag 120
agcaggaaga tggtcattcc caacaccaga tgcaggcgga agacgaacgc tacgccgttg 180
agcatctctg acgatccacc acggaagtga a 211

<210> 23
<211> 154

<212> DNA
<213> Escherichia coli

<400> 23
cacgacggat tttcgtgcc atgattcgct ccttagagta cttctggtgc cagagagata 60
attttcatga acttctcact acgaagctca cgagttaccc ggcccaaaa tacgcgtacc 120
gataggctgc tcgctgttgt tggtcagaag aaca 154

<210> 24
<211> 160
<212> DNA
<213> Escherichia coli

<400> 24
acttcgtcat cacgacggat tttcgtgcc atgattcgct ccttagagta cttctggtgc 60
cagagagata attttcatga acttctcact acgaagctca cgagttaccg gcccaaaaat 120
acgcgtaccg ataggctgct cgctgttgtt gttcagaaga 160

<210> 25
<211> 244
<212> DNA
<213> Escherichia coli

<400> 25
aatgaccttg ccggaagaca ggacattctt aactttaccg cgtttacctt tatctttacc 60
ggttaacacg ataacttcgt catcacgacg gattttcgct gccatgattc gctccttaga 120
gtacttctgg tgccagagag ataattttca tgaacttctc actacgaagc tcacgagtta 180
ccggcccaaa aatacgcgta ccgataggct gctcgctggt gttgttcaga agaacacaag 240
catt 244

<210> 26
<211> 108
<212> DNA
<213> Escherichia coli

<400> 26
tgttcgatct cgaaacttac acctttctca gccagcacaa tgcggacctg atggctatag 60
atgtcagtag gaccggaaaa cagcgtcatt acccgaacgt ttgttggc 108

<210> 27
<211> 369
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 27
tccagacgct ctttcttggc gtcgtagtca aagatacccc ctaagaacgt cggagcggtc 60
cgtgagtcct gaatgcgatt atttaccgga ttaatttcaa acatggctctg atttctttta 120
ttgagctagt caaaatgcgg tgataagagc gggattgtac ccaatccacg ctctttttta 180
tagagaagat gacgctaaat tggccagata ttgtcgatga taatttgag gctgcgggtc 240
cacgaaactc gttgatatcg agcttataag ccagttgcac ttngcgcacc cgttatccgg 300
ccagagggcg gtatcgacat taaaagcaat accatccagc agtggaccgc cgcccgaccg 360
gttcgacca 369

<210> 28
 <211> 457
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(457)
 <223> n = A,T,C or G

<400> 28
 accccctaag aacgtcggag cgttccgtga ggtcctgaat gcgattatTT accggattaa 60
 tttcaaacaT ggtctgattt cttttattga gctagtcaaa atgcggtgat aagagcggga 120
 ttgtacccaa tccacgctct tttttataga gaagatgacg ctaaattggc cagatattgt 180
 cgatgataat ttgcaggctg cggttgccgc gaaactcgtt gatatcgagc ttataagcca 240
 gttgcacttc gcgcacgccg ttatccggcc agagggcggt atcgacatta aaagcaatac 300
 catccagcag tggaccgccg ccgaccggtt cgaccatnac cttcaaataga cgttcgcccc 360
 ccagccgctg ttgcancaga cggaaatgac cgtcaaacag cggctccggg aacatctgcc 420
 cccacggggc agcatcgcgC agcagctgcg ccacttc 457

<210> 29
 <211> 729
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 29
 ctttttacgg acaaacaatc atgcaaccag aagttgaagt attaacccgat cataatgagc 60
 taatttgttc gagctttatt gaacacattg ccaacacatt aaatttagga gtggtgtaca 120
 actaaacctg cagccaagga tgtatagtga gcgaagccct atcaggcctt tttggtcagt 180
 agataagatt gatcttcgtt gatagaattt acttacacca gctgttacat taagataatt 240
 ttttggtggg agaatgataa gatcttacgt aacaatttga ttttaatggt gccgataata 300
 ggagtcgaac ctacgacctt cgcattacga atgcgctgct ctaccaactg agctatatcg 360
 gccctgaaag gacatgttca cgaacgtgaa tcacggtgga caagggtaaa actaaccggg 420
 cgatgcgtca atggccttgt gaatcaaata gctacttttg catcaccggg ttttatTTac 480
 gcacgaatgg tgtaatcacc aatgccgatc cacttgtaag tggTcaagt cttncagccc 540
 cattgggccca cgcgccgtgg agttttttgtg tgcttaccgg cactttcgca cccagaccaa 600
 actggccgcc gtcggtaaaa cgcgtagagg cgttacgtaa acagcggacg aatccacttc 660
 gtnacaaaac gcttggcggtT ggcatatcgc gggtcangat cgcaatcgga gtgtttgtgtg 720
 cccgggttn 729

<210> 30
 <211> 305
 <212> DNA
 <213> Escherichia coli

<400> 30
 agccattgtc cggagaatTT tCGtctttct cgagggtatt atctgaaagt aactcttctg 60
 agctagagtc ttctatgttt aaatccatag tataattaat ttgggggacg accagataag 120
 cattttcttt ggtattttca taatcttcaa tgattatata cgatgtaata atatattttt 180
 tctgatgaga attctttcat ctctgttaat ttaattctgt tcaagcaatt gatgattttc 240
 gatgagcttt tatatatTTc ttttgTTaat tcatttttcta atttatctgt aagagttgcc 300

cttgg

305

<210> 31
<211> 425
<212> DNA
<213> Escherichia coli

<400> 31
agggttactgg cgagggttatc gagaaacgcc agactgatac ccataaaaaa gagaataaagg 60
taaaccatcc agcttaatag ctgattaata acttttaacg cagcttggtg gcgaagcgga 120
atgaggtaac ccacaatcag gggaaccaga atgattaaca gccagaaaaa catgaaaacc 180
cagtccttgc aaagatgaag tcgaaatgcg cgatgacaca ctactgaaag cggaaggacg 240
agtaaagttg caattaaaag gaaatgttat gcataaggag cagtagagta ttcgttttca 300
tttaaagata ttcttgcgct ttaattacaa actgcaccga tgttggtggc gtcaaaatcg 360
ccgaggcggt ccctgaaggc cggggcagcc cacatggatg tgggctgagg gcgcgtttta 420
caggg 425

<210> 32
<211> 381
<212> DNA
<213> Escherichia coli

<400> 32
aaaagagaat aaggtaaacc atccagctta atagctgatt aataactttt aacgcagctt 60
gttggcgaag cggaatgagg taaccacaaa tcaggggaac cagaatgatt aacagcccag 120
aaaacatgaa aaccagtcct ttgcaaagat gaagtcgaaa tgcgcgatga cacactactg 180
aaagcggaaag gacgagtaaa gttgcaatta aaaggaaatg ttatgcataa ggagcagtag 240
agtattcggt ttcatTTaaa gatattcttg cgctttaatt acaaactgca ccgatgttgg 300
tggcgtcaaa atcgccgagg cgttccctga aggccggggc agcccacatg gatgtgggct 360
gagggcgcggt ttacagggga t 381

<210> 33
<211> 329
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(329)
<223> n = A,T,C or G

<400> 33
gtcgaagtgtg tgcccgaact tgccatgctc cagtcctttt cttctggggc gactttccgg 60
gaggtgctta aacgaaaaaac cccgcccggt ttgcgcgggc ggggttttgg aatcgtgtgt 120
tgttccagtc cctacggcgc attgccgacg accaccaoca cagcacgac gaccactgcg 180
gcggatgggc gcagttggta gtagttttgc gttgagcatg gaagtagtca ttggggacct 240
tgttggtttt gtgtttaaca atatTTatac aagcacagct ttacagggga gacaatggaa 300
aatttttcag caagggaaaa ttgaggggn 329

<210> 34
<211> 442
<212> DNA
<213> Escherichia coli

<400> 34
gatgttgtgc ccgaacttgc catgtccag tccttttctt ctgggccgac tttccgggag 60
gtgcttaaac gaaaaacccc gcccggttg cgccggcggg gttttggaat cgtgtgtgtg 120

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tccagtcacct acggcgccatt gccgacgacc accaccacac gcacgacgac cactgcgggcg 180
gatggcgccag ttggtagtag ttttgcggtg agcatggaag tagtcattgg ggaccttggt 240
ggttttgtgt ttaacaatat ttatacaagc acagctttac aggggagaca atggaaaatt 300
tttcagcaag ggaaaattga ggggttgatc acgttttgta ctgaattgca gataacaaaa 360
aaccgcgccg gacgaggtt tcgtcagtcg cctgcggtg gtaaccgcaa agcacactgt 420
attatgtcaa cactgaaagt at 442
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<210> 35

<211> 272

<212> DNA

<213> Escherichia coli

<400> 35

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cgattatagg gctgaccaa tacatggata gataatatgc catcccccca ggcagtccac 60
gtaaaaagag catatacaag gagaatagaa cacctacagc tgtaataaga taaacataat 120
gttttactct attaacacct acgatgaatg cataagagat gataaccata aagacaattt 180
gcttaccagt attcagtata attgcaaaga tgaatacaat aaaaacaagt aaagtaaattg 240
ttttacttac ctttgtatta gtaaattttt ta 272
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<210> 36

<211> 255

<212> DNA

<213> Escherichia coli

<400> 36

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tgcgattacg gcatgcttat gatcaggaat gttaatgcct gctatacggg ccactatgca 60
ctcctactat ttaatatgta cgttccatgc tgaaaagccc gttttcagga tactcaaattg 120
gaaacgcaca gacatacaaa agattggctg gctaattctag ccagctcaac ccaactttgc 180
aagaaaaata tgcgaaaaaa tcagccttgg cgctgtttat gcttcggctc ggcactgcaa 240
atcacacgga tgaca 255
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<210> 37

<211> 389

<212> DNA

<213> Escherichia coli

<400> 37

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aacgtaaaac tttacgtaaa ttaacatggt taacattttat gccactattg tttgtaaatt 60
catatttcgt aatgcttctg aatttttcgt gtgatggttt taaatactat ggtgtttact 120
cttgagggga cggcctatct ataaaatacg gacatttcaa taaatgcccg tataaacaga 180
gtatgattct ggctggctcg tgagtatcaa tgttgaccg aatgtgaacg aataaataat 240
tcgtttatct taccacccat tctcttttcg attcgttgct tgtacgcgta gatgctacgg 300
atatccatat ccagaacttc agcaatctga tatggattat aaccagaaac catatacccc 360
attatggtga attccatctg agttaatgt 389
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<210> 38

<211> 178

<212> DNA

<213> Escherichia coli

<400> 38

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gtgggttagga tctttatagt tacgctcggc ggcatccatc gggatacctg cggcattttc 60
tttgcaaaaa ccgatttcag aattgtgttt gtttgatga acctgaatgg agagtggctg 120
tgctgcgcat aatactttga acaggaaagg cagttcgcca aagcgtttgg caacggcc 178
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<210> 39

<211> 191

<212> DNA
<213> Escherichia coli

<400> 39
tcgcaaggaa aggcgtcagc gcaaaaacca gctccggctt gtgggtagga tctttatagt 60
tacgctcggc ggcattccatc gggatacctg cggcattttc ttgggcaaaa ccgatttcag 120
aattgtgttt gtttggaatga acctgaatgg agagtggctg tgctgcgcac aatactttga 180
acaggaaagg c 191

<210> 40
<211> 158
<212> DNA
<213> Escherichia coli

<400> 40
ccggcttggtg gttaggatct ttatagttac gctcggcggc atccatcggg atacctgcgg 60
cattttcttt ggcaaaaccg atttcagaat tgtgtttgtt tggatgaacc tgaatggaga 120
gtggctgtgc tgcgcataat actttgaaca gaaaaggc 158

<210> 41
<211> 184
<212> DNA
<213> Escherichia coli

<400> 41
tcgaagaatt taacggaggg taaaaaaacc gacgcacact ggcgtcggct ctggcaggat 60
gtttcgtaat tagatagcca ccggcgcttt aatgcccggg tgcggatcgt agccttcaat 120
ctcaaagtct tcgaaacggt agtcgaagat ggattcgggt ttacgtttga taatcaactt 180
cggc 184

<210> 42
<211> 122
<212> DNA
<213> Escherichia coli

<400> 42
gtagaagttc aaattacgaa cctgaatttt actcggggca gtttcaacca tactcattgc 60
aatcttttcc tcatcgtgcc tgatgcactt cgctaatacag gcttaccgta ggccgggatca 120
gg 122

<210> 43
<211> 163
<212> DNA
<213> Escherichia coli

<400> 43
taaattccgc gtatagcgtg ggcgcttttg ctccgggtgc ttccgacgagg tccgcaagag 60
aagtcgcttc ataaccgtgt tgccagaaca atttcatggc cttatcaagc gcggcatccc 120
tgtcgaacac ttttggggcg ccacggcttt tttttacaca ttg 163

<210> 44
<211> 161
<212> DNA
<213> Escherichia coli

<400> 44
gcaaattgttt tcgtaattca ggagaaatgg caaataaagc attaaaaatt tgaatgcttt 60

<222> (1)...(300)
<223> n = A,T,C or G

<400> 49
agctgatcga tgggtgtttgc caacgcacac gccaccgcgg cggcggcaaa caccancgta 60
ccgccgagca ccaccggctt acgcccgaag ctgtctgccca tcggcccgtg gattaactgc 120
cccaacgcaa agcccagaat ataagtactg agggatcatct gcgtactgcc cgnccggtacg 180
ccaaactgcg ctgaaattac cggtagcgcg ggcagatata tatcaatcga cagcggcatc 240
aacatggcca gcaggccaag gataaaaaca atagcaaacg acgaatgctg tcgggtggtc 300

<210> 50
<211> 207
<212> DNA
<213> Escherichia coli

<400> 50
caacatctca tgtctggatt ttagatata cgtggaattc caattggtat cttttgtagg 60
attcaacata tcatgtaagc gctgggagct taccaccata actggcccat catcgactga 120
ggagaacagg ataaagatat tatcgtttcg tgtaattca ttcgtgttaa aggttcttaa 180
attatcttca gtttctataa atatagg 207

<210> 51
<211> 213
<212> DNA
<213> Escherichia coli

<400> 51
ttctgtaatc agaaaaagaa gaactggaat ttaataaat attatttctc tgggaacggg 60
ggggataaat caatatgacg agttgaatat tatatttttt ataagaatta tatgagatta 120
aagaaatctg ccgtaaagac agatttcttt aaaagataat tagagatttg cgacgttatg 180
ataaactttt tgtacatcgt cgtcatcttc aag 213

<210> 52
<211> 381
<212> DNA
<213> Escherichia coli

<400> 52
tctgttagtg tattatccac tgcggccctt tccgccgtct cgcaaacggg cgctggcttt 60
aggaaaggat gttccgtggc cgtaaatgca ggtgtttcac agcgttgct atcgcggcaa 120
tatcgccagt ggtgctgtcg tgatgcggtc ttcgcatgga ccgcacaatg aagatacggc 180
gcttttgtat cgtacttatt gtttctgggt cgctgttaac cgaggtaaat aataaccgga 240
gtctctccgg cgacaattta ctgggtggta acaaccttca gagcagcaag taagcccga 300
tgccgccctt tgggcggcat attttagatt atccgattct gtttaaagtc acgcaaaaaa 360
ccaccccgac gacgttcata g 381

<210> 53
<211> 154
<212> DNA
<213> Escherichia coli

<400> 53
aaatagaccg gcatactttc gtgcggcagc ataataca gtacgagcgc agcggacta 60
atgataaagg ttagcatag atatttactt ggcgatttca ggatcttatt tgaaatcatg 120
ccaccaatcg gtccaccaat cattttcaga cagt 154

GGTGTGTTGC

<210> 54
 <211> 191
 <212> DNA
 <213> Escherichia coli

<400> 54
 tccttagtca ggtactgacg tacttttaaaa tcgctgtcca ggttgtcagc gaattctttg 60
 gtgttcgcaa accaggtaga gttccatggt tttacaatac ccaggcgaat accattagga 120
 tgtactttct gacccattgc tagtctccag agtctcagcg atcggacaca accacagtga 180
 tgtggctggg g 191

<210> 55
 <211> 190
 <212> DNA
 <213> Escherichia coli

<400> 55
 gctgggtgcc gttttccatg ccagtggggc gacgcgcggc aaggcactat ccggcaaggg 60
 ttgcgcttca tcagccataa tccggcgaat gatccacgcc gccccgcagc acattaaagg 120
 ccgttcaagc agcggatcgt caggctgtaa gcgcaatttg cctgccttgc cgtggcgagc 180
 aaacgcggta 190

<210> 56
 <211> 402
 <212> DNA
 <213> Escherichia coli

<400> 56
 aaaaaatgaa attcctcttt gacggggcaa tagcgatatt ggccatTTTT ttagcgcaac 60
 atttgcgga aattcccttc tccatacagg tgtagtgcac cgaccgcgac cacatatcgc 120
 cccggcgga tggcggttaa tttatccgc caggcgagat ttcgctgatg catcagcaca 180
 tcgtacagcg actgactgaa cgtattgggc agcgttatat cattatTTTg cggcggtgca 240
 ttcagccacc agctcatcat ttgttgcagc aaccgtgcgt tggatgcca gtgggtcagc 300
 gtatcgcca gcagcgccag tcctttgtca gggagctgga gcaacatggc aatctggttt 360
 tcagccctt ccagttcaat cacgggttta tggtgttgc tc 402

<210> 57
 <211> 595
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 57
 aattaatcag agcaacggta aaacaatgaa agtgtaaaaa acacttttgc gccattatg 60
 gagaaaaaaa gaaaatttga tggagagtga tgagagaata ttacaacacg atgattttgc 120
 agagattatg aagaactata ccgatgact ggtgataaat aaagcaaata accaggatta 180
 atctgtatta atttataaga aagcaactta ataccgcag aatgatttct gcgggtaagt 240
 attagcttat ttttcgagc attaatcccg cgcgtaatcc caacgctacc aacggattag 300
 ggaataacac atactctaca tcatgggtta cggtaaaacg ttcctctccg tcctgcgcca 360
 gcaatgttcc tttctcaaac ggcataaaat tcagcgtgtc acttgccata tgcatttcga 420
 aggacggcga gtggcgagta atttgcgaaa ccacccgata acggagcggc ggtgttctca 480
 cgataccgac actctcacca gatagcagcg cagcaattgc gctggcagtt actgcaaact 540
 ggcgaagatc gttttgccca aagggaacg ctttgccaag ttncagccgt acang 595

<210> 58
 <211> 250
 <212> DNA
 <213> Escherichia coli

<400> 58
 gaaactcagt ggaatggggg agccgcaata gcgaacatgt tccatgccgc caataatctg 60
 tgcgcggtga atatgcccga gcgcgatgta gtcggctggg ggaaagtgtt gtgccggaaa 120
 cgcgccagc gtgccaatat aaatgtcacg cacggcgta cttttactgg ccccccacgg 180
 cgttaaatgt cccgtggcga tgatgggcag aggtgatcg ccgcgcagtt tgcaggcatc 240
 ggcatagtgt 250

<210> 59
 <211> 236
 <212> DNA
 <213> Escherichia coli

<400> 59
 aaaggttcgg caaaagccat aaccttttcg tcagctttgg ccggataagg gacacattgc 60
 gacgtttcga ccattttata acgggtaaaa ccaccatcaa catgaggaa atacatggca 120
 ctgccaaaaa aacgcataac tgtacactga ttctcggtat gttcaatgca gtatttgcag 180
 tgaccgcacg gtttagacgg attaatggct accgtttgcc cttcatgtaa ttctga 236

<210> 60
 <211> 92
 <212> DNA
 <213> Escherichia coli

<400> 60
 gaagagatgt tcaggttttc gttatcggca atggtatcga acttgatatt ctcatatttc 60
 tcgtcaggcg tggagtacgc cgccgcacg aa 92

<210> 61
 <211> 62
 <212> DNA
 <213> Escherichia coli

<400> 61
 tgtcgacatt cagcatttc ggtattcgt cgccgagggc aaatgtacag gttgaggagg 60
 tg 62

<210> 62
 <211> 72
 <212> DNA
 <213> Escherichia coli

<400> 62
 acttatcaaa ccatttttcc gttcaccgg aggtctgcac ctgagcgatg gtgtcatcca 60
 tcagctttt ga 72

<210> 63
 <211> 66
 <212> DNA
 <213> Escherichia coli

<400> 63

gcaacttgnt ggacagggca aaaaattcct gcctgggtcg ccgnatctgn g 531

<210> 68
<211> 102
<212> DNA
<213> Escherichia coli

<400> 68
agcgccggtta acgcccgtta aatgttctcg ttcggttcc cgatcgttat tcaacaggct 60
gcgtaccgta gcggcatatt tcttccctgc ttcacgcca tc 102

<210> 69
<211> 167
<212> DNA
<213> Escherichia coli

<400> 69
aaaactcacc ttttttgttg ttatccctca attaccacaa gtaaaaggag ataaaccgac 60
aatgacctag acgtaattat gtaaaaatac tgatgttcgt cactgactat ttccgatatt 120
cagctgttga aaaatcaaaa aactggaaaa ataattttaa atatcat 167

<210> 70
<211> 83
<212> DNA
<213> Escherichia coli

<400> 70
gccacgcca gcataaacag cgggatcgag ccttcaatcg gtacgcccag tacacctttc 60
accatcagca ccagcgataa tcc 83

<210> 71
<211> 103
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(103)
<223> n = A,T,C or G

<400> 71
gccnggcggg aaccgacatg ttccactct acgcccgtcg gcgcggtttt catttttgcg 60
cacctgatag ccgcacgatt gcagatcaac aacgcctttt ttg 103

<210> 72
<211> 121
<212> DNA
<213> Escherichia coli

<400> 72
tagcttcttc cacattgtcg aactgaacgt ccagacgggtg tttagaaacg ttgatgctcg 60
ggattttttc cgcaccacgg caaacgcgcg ccatggctgc aacggtttct gacggatact 120
g 121

<210> 73
<211> 163
<212> DNA

<213> Escherichia coli

<400> 73

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tagttattgg ctgttttgag aatgtaatct tccaactgct tataactctt cagatgcaat 60
aatccgagaa tcacatgcaa tttattcata aattcgtggg atcgttcacg aagtgcgtca 120
gcatagtga ccagaccgtc gagtcgctgc atcagtttac gta 163
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<210> 74

<211> 106

<212> DNA

<213> Escherichia coli

<400> 74

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aaaaccatga ggttattatg gccgatttga ggagggaaag agtaagagca gtttggttaa 60
tgtacaacga cgattctccc accgggcgcg ttttaaagcg acggtg 106
```

<210> 75

<211> 319

<212> DNA

<213> Escherichia coli

<400> 75

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ctggagattg agtagatatt cttgttcaga atgtatcagc ccgatgggtc tacgattctt 60
aagccacgaa gagttcagat agtacaacgg catgtctctt ttgactatct ggcaaccg 120
cagtgtgttc tctcacgcat cacaaaagca gcaggcataa aaaaaccg 180
ttttcacaaa gtttcagcaa attggcgatt aagccagttt gttgatctgt gcagtcaggt 240
tagccttatg acgtgcagct ttgtttttgt ggatcaaacc tttagcagcc tgacgggtcca 300
cgatcggttg catttcgtt 319
```

<210> 76

<211> 237

<212> DNA

<213> Escherichia coli

<400> 76

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cgaaccaacg acccccacca tgtcaagggtg gtgctctaac caactgagct atgaacgcaa 60
cgttgtaggt gacaacgggg acgaatatta gcggcagagt gggaagggtg caagaggcaa 120
aacgtaattt tctgcgctat ttcgaccgtt tgcagagctt ttaagcaa at tggctatatt 180
ttgttgattt gcaagggtga tttttattca ggatcgcatt tacatctgat acaaccc 237
```

<210> 77

<211> 241

<212> DNA

<213> Escherichia coli

<400> 77

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tgtgacagag tggttatcgt taatcaggca aagagggaaa aacatattat ttaaaccatt 60
atagcgcata aaatatcctt ataattaaca agaaagaaaa ggcatattct ctgcattatc 120
attttctacg actgtcaaaa atcgctcatt ttttaatgag tttatttggt taatattatg 180
ggaaaagggtg atgcatttgg gagaggaaga gtattccccg gtcagacgac cggggaagg 240
g 241
```

<210> 78

<211> 89

<212> DNA

<213> Escherichia coli

<210> 84
 <211> 632
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(632)
 <223> n = A,T,C or G

<400> 84
 tnnccannnnc nnnnnnnnnn nnnnnnnncn ntncctagan tntcnangtc tncnncnncn 60
 tnnccnnncc cttcnnnncc nnnnnanangn nnnnncccc cnnnccnnt tttgttttgg 120
 aaantccgtt tcaggaanag cttctgaatc ccganccgntt gataactgnn ggccagagtc 180
 ataatgcgca ccaataataa tcagcgggcc atcggcagga ccataatcag caacaatgnn 240
 nnggtagggg ccacccgtaa tggggaccgt cctgcgaggt aactctggca ccgctactga 300
 caaagacctc ttttatatat tctgcgggac ctattcagat tatcaatatt gtcnggcact 360
 acgtggatgc acaagtttgt gtaagataac gaactgnttt ttctaattgc tcaggacttt 420
 gcgtgtcggg gccgttgacg gtaatgcatt gaccaggggt tggtaaaaaa taatcatagg 480
 gagtaaaaaa acaataataa taataaaagc caagattatt tttttcatat gcaaaaattat 540
 taatgggggt gcgtttgggt aatcattatn ttgctatggg tttcgatatt gngattttta 600
 ttaaagatta agcangggat tataccaaaa ga 632

<210> 85
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 85
 gcgtatttca gcgtaattgg cagcagctgc ggatcgctcat caatcttctc tgacagcggc 60
 tgatgtactt caaccagacg cgcaccgttt ggttcggcag agacttttat cggagtgttg 120
 atgatattca ctttggtgcc tggggtgacc tggctaaaga g 161

<210> 86
 <211> 188
 <212> DNA
 <213> Escherichia coli

<400> 86
 caagggtgag catttgcagc gaatcagaaa gggcgcagaa cagtgaagac aacagaaaaa 60
 cgaccagacc gcatttataa atacgtcgat agccaaacat atcgcccaga aacgaaaacg 120
 agagcagga gatgacaatg gcgatttgat aggcgttcac taccagatg gaactggctg 180
 gcgtggca 188

<210> 87
 <211> 175
 <212> DNA
 <213> Escherichia coli

<400> 87
 tgagcatttg cagcgaatca gaaagggcgc agaacagtga agacaacaga aaaacgacca 60
 gaccgcattt ataaatacgt cgatagccaa acatatcgcc cagaaacgaa aacgagagca 120
 gggagatgac aatggcgatt tgataggcgt tcactacca gatggaactg gctgg 175

<210> 88
 <211> 194
 <212> DNA

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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cgcaaggggtg agcatttgca gcgaatcaga aagggcgcgag aacagtgaag acaacagaaa 60
aacgaccaga cgcatttat aaatacgtcg atagccaaac atatcgccca gaaacgaaaa 120
cgagagcagg gagatgacaa tggcgatttg ataggcgttc actaccaga tggaactggc 180
tggcgtggca tgaa                                     194

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<211> 272

<213> Escherichia coli

ccttgataaa	ggaaaagggtt	atgatgaagc	tctgcatcat	actggttggtg	ttgttactgt	60
taagtttccc	gacttactaa	caactcatca	gaggggggag	aaatcctccc	ttacccttgt	120
tcctttactc	taggttgaag	aaacaacagc	gtcaataggc	ctgccatgta	cgaagcgaga	180
tctgtgaacc	gctttccggt	tagecctttt	tatcctgttg	gatcttcttg	atgatgttgg	240
tcgtcgagca	accgtcttca	aagttgaqca	cc			272

<211> 245

<213> Escherichia coli

ccttgataaa	ggaaaaggggt	atgatgaagc	tctgcatcat	actggttggt	ttgttactgt	60
taagtttccc	gacttactaa	caactcatca	gaggggggag	aaatcctccc	ttacccttgt	120
tcttttgaac	taggttgaaa	aaacaacagc	gtcaataggc	ctgccatgta	cgaagcgaga	180
tctgtgaacc	gctttccggg	tagccttttt	tatcctgttg	gatcttcttg	atgatgttgg	240
tcgtc						245

<211> 203

<213> Escherichia coli

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taccaaaaaa agccacgtta tctgtttgat gcaaaagagt gaacgtggcg ttaaattgtaa 60
ccagttatat cagtagaaaa cctggttgtt gttaacagtc taaccggtca attttttatg 120
atttttttga taaaaattaa attttatttg cttaatacac caccagatga cgttcgccat 180
ccagggcttg aacctgaagt tta                                     203
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<211> 189

<213> Escherichia coli

<221> misc feature

 $\langle 222 \rangle \quad (1) \dots (189)$

<223> n = A, T, C or G

ctaatagactt attttctgct taccaaaaaa agccacgtta tcttgttgat gcnaaagagt 60
gaacgtggcg ttaaatgtac cagttatatt agtagaaaac ctggttgntg ntaacagtct 120
aacccggcaat tttttatgat ttttttgata aaaattaaat tttatttgct ttaatcacca 180

ccagatgac

189

<210> 93

<211> 221

<212> DNA

<213> Escherichia coli

<400> 93

agcgcaacag cggaaccag ggtagccagt ttttcatgt tcatattcaa gatgtcctgt 60
agtcgttatt actgcttttt gttgtctacc agcaccgcca gcaaaatcac caccgctttg 120
acgatcatct ggtaatagga ggaaacacct aacaaattca atccattatt aaggaagcca 180
agaattaatg cgccgatcaa cgtcccaaca atgcgacctt t 221

<210> 94

<211> 117

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(117)

<400> 94

atg aaa gtt cgt gct tcc gtc aag aaa tta tgc cgt aac tgc aaa atc 48
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1 5 10 15

gtt aag cgt gat ggt gtc atc cgt gtg att tgc agt gcc gag ccg aag 96
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
20 25 30

cat aaa cag cgc caa ggc tga 117
His Lys Gln Arg Gln Gly *
35

<210> 95

<211> 1332

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1332)

<400> 95

atg gct aaa caa ccg gga tta gat ttt caa agt gcc aaa ggt ggc tta 48
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1 5 10 15

ggc gag ctg aaa cgc aga ctg ctg ttt gtt atc ggt gcg ctg att gtg 96
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
20 25 30

ttc cgt att ggc tct ttt att ccg atc cct ggt att gat gcc gct gta 144
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
35 40 45


```

ggg gta atc ccg gca atc ttc gct tcc agt att att ctg ttc ccg gcg      864
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
      275                      280                      285

acc atc gcg tca tgg ttc ggg ggc ggt act ggt tgg aac tgg ctg aca      912
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
      290                      295                      300

aca att tcg ctg tat ttg cag cct ggg caa ccg ctt tat gtg tta ctc      960
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
      305                      310                      315                      320

tat gcg tct gca atc atc ttc ttc tgt ttc ttc tac acg gcg ttg gtt      1008
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
      325                      330                      335

ttc aac ccg cgt gaa aca gca gat aac ctg aag aag tcc ggt gca ttt      1056
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
      340                      345                      350

gta cca gga att cgt ccg gga gag caa acg gcg aag tat atc gat aaa      1104
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
      355                      360                      365

gta atg acc cgc ctg acc ctg gtt ggt gcg ctg tat att acc ttt atc      1152
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
      370                      375                      380

tgc ctg atc ccg gag ttc atg cgt gat gca atg aaa gta ccg ttc tac      1200
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
      385                      390                      395                      400

ttc ggt ggg acc tca ctg ctt atc gtt gtt gtc gtg att atg gac ttt      1248
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
      405                      410                      415

atg gct caa gtg caa act ctg atg atg tcc agt cag tat gag tct gca      1296
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
      420                      425                      430

ttg aag aag gcg aac ctg aaa ggc tac ggc cga taa      1332
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg *
      435                      440

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<210> 96
 <211> 435
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(435)

<400> 96
 atg cgt tta aat act ctg tct ccg gcc gaa ggc tcc aaa aag gcg ggt 48
 Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly

145	150	155	160	
ggt gaa gaa att ctg ggg aaa taa				504
Val Glu Glu Ile Leu Gly Lys *				
	165			

<210> 99
 <211> 354
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(354)

<400> 99	
atg gat aag aaa tct gct cgt atc cgt cgt gcg acc cgc gca cgc cgc	48
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg	
1 5 10 15	
aag ctc cag gag ctg ggc gca act cgc ctg gtg gta cat cgt acc ccg	96
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro	
20 25 30	
cgt cac att tac gca cag gta att gca ccg aac ggt tct gaa gtt ctg	144
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu	
35 40 45	
gta gct gct tct act gta gaa aaa gct atc gct gaa caa ctg aag tac	192
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr	
50 55 60	
acc ggt aac aaa gac gcg gct gca gct gtg ggt aaa gct gtc gct gaa	240
Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu	
65 70 75 80	
cgc gct ctg gaa aaa ggc atc aaa gat gta tcc ttt gac cgt tcc ggg	288
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly	
85 90 95	
ttc caa tat cat ggt cgt gtc cag gca ctg gca gat gct gcc cgt gaa	336
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu	
100 105 110	
gct ggc ctt cag ttc taa	354
Ala Gly Leu Gln Phe *	
115	

<210> 100
 <211> 534
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1)...(534)

<400> 100

atg tct cgt gtt gct aaa gca ccg gtc gtt gtt cct gcc ggc gtt gac 48
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1 5 10 15

gta aaa atc aac ggt cag gtt att acg atc aaa ggt aaa aac ggc gag 96
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
20 25 30

ctg act cgt act ctc aac gat gct gtt gaa gtt aaa cat gca gat aat 144
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35 40 45

acc ctg acc ttc ggt ccg cgt gat ggt tac gca gac ggt tgg gca cag 192
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50 55 60

gct ggt acc gcg cgt gcc ctg ctg aac tca atg gtt atc ggt gtt acc 240
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65 70 75 80

gaa ggc ttc act aag aag ctg cag ctg gtt ggt gta ggt tac cgt gca 288
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85 90 95

gcg gtt aaa ggc aat gtg att aac ctg tct ctg ggt ttc tct cat cct 336
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100 105 110

gtt gac cat cag ctg cct gcg ggt atc act gct gaa tgt ccg act cag 384
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115 120 125

act gaa atc gtg ctg aaa ggc gct gat aag cag gtg atc ggc cag gtt 432
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130 135 140

gca gcg gat ctg cgc gcc tac cgt cgt cct gag cct tat aaa ggc aag 480
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145 150 155 160

ggt gtt cgt tac gcc gac gaa gtc gtg cgt acc aaa gag gct aag aag 528
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165 170 175

aag taa 534
Lys *

<210> 101

<211> 393

<212> DNA

<213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(393)

<400> 101

atg agc atg caa gat ccg atc gcg gat atg ctg acc cgt atc cgt aac	48
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn	
1 5 10 15	
ggt cag gcc gcg aac aaa gct gcg gtc acc atg cct tcc tcc aag ctg	96
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu	
20 25 30	
aaa gtg gca atc gcc aac gtg ctg aag gaa gaa ggt ttt att gaa gat	144
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp	
35 40 45	
ttt aaa gtt gaa ggc gac acc aag cct gaa ctg gaa ctt act ctg aag	192
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys	
50 55 60	
tat ttc cag ggc aaa gct gtt gta gaa agc att cag cgt gtc agc cgc	240
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg	
65 70 75 80	
cca ggt ctg cgc atc tat aaa cgt aaa gat gag ctg ccg aaa gtt atg	288
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met	
85 90 95	
gcg ggt ctg ggt atc gca gtt gtt tct acc tct aaa ggt gtt atg act	336
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr	
100 105 110	
gat cgt gca gcg cgc cag gct ggt ctt ggt ggc gaa att atc tgc tac	384
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr	
115 120 125	
gta gcc taa	393
Val Ala *	
130	

<210> 102
 <211> 306
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(306)

<400> 102

atg gct aag caa tca atg aaa gca cgc gaa gta aaa cgc gta gct tta	48
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu	
1 5 10 15	
gct gat aaa tac ttc gcg aaa cgc gct gaa ctg aaa gcg atc atc tct	96

Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser	
20 25 30	
gat gtg aac gct tcc gac gaa gat cgt tgg aac gct gtt ctc aag ctg	144
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu	
35 40 45	
cag act ctg ccg cgt gat tcc agc ccg tct cgt cag cgt aac cgc tgc	192
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys	
50 55 60	
cgt caa aca ggt cgt ccg cat ggt ttc ctg cgg aag ttc ggg ttg agc	240
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser	
65 70 75 80	
cgt att aag gtc cgt gaa gcc gct atg cgc ggt gaa atc ccg ggt ctg	288
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu	
85 90 95	
aaa aag gct agc tgg taa	306
Lys Lys Ala Ser Trp *	
100	

<210> 103
 <211> 540
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(540)

<400> 103	
atg gcg aaa ctg cat gat tac tac aaa gac gaa gta gtt aaa aaa ctc	48
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu	
1 5 10 15	
atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag	96
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu	
20 25 30	
aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa	144
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys	
35 40 45	
ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa	192
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys	
50 55 60	
ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt	240
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg	
65 70 75 80	
cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg	288
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met	
85 90 95	

Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
85 90 95

aag tct aac agc gaa act atc aag taa 315
Lys Ser Asn Ser Glu Thr Ile Lys *
100

<210> 105
<211> 372
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(372)

<400> 105
atg atc caa gaa cag act atg ctg aac gtc gcc gac aac tcc ggt gca 48
Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
1 5 10 15

cgt cgc gta atg tgt atc aag gtt ctg ggt ggc tcg cac cgt cgc tac 96
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
20 25 30

gca ggc gta ggc gac atc atc aag atc acc atc aaa gaa gca att ccg 144
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
35 40 45

cgt ggt aag gtc aaa aaa ggt gat gtg ctg aag gcg gta gtg gtg cgc 192
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
50 55 60

acc aag aag ggt gtt cgt cgc ccg gac ggt tct gtc att cgc ttc gat 240
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65 70 75 80

ggt aat gct tgt gtt ctt ctg aac aac aac agc gag cag cct atc ggt 288
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
85 90 95

acg cgt att ttt ggg ccg gta act cgt gag ctt cgt agt gag aag ttc 336
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
100 105 110

atg aaa att atc tct ctg gca cca gaa gta ctc taa 372
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu *
115 120

<210> 106
<211> 1458
<212> DNA
<213> Escherichia coli

<220>

<221> CDS
 <222> (1)...(1458)

<400> 106

gtg gga att tat ttt act aat tca gat gat caa att tac ttt aaa agg	48
Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg	
1 5 10 15	
agt gaa ggg atg tct gat ata aac cat gca ggt tct gac ctt ata ttt	96
Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe	
20 25 30	
gaa ctg gag gat cgc cct ccc ttt cat cag gct ctc gtt ggt gcc att	144
Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile	
35 40 45	
acc cat ctg ttg gca att ttc gtt ccg atg gta acc ccc gcg tta atc	192
Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile	
50 55 60	
gtg ggt gcg gcc tta cag ctt tcc gct gaa aca act gcc tat ctt gtt	240
Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val	
65 70 75 80	
tct atg gcg atg atc gcc tct ggt att ggt acc tgg tta caa gta aac	288
Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn	
85 90 95	
cgc tac ggc atc gtc ggt tct ggc cta ctc tca att cag tca gtc aat	336
Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn	
100 105 110	
ttt tca ttt gtt acg gtc atg att gcg ctg ggc agc agc atg aaa agc	384
Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser	
115 120 125	
gac ggt ttt cac gaa gag tta atc atg tgc tgc ctt ctc ggc gtc tcc	432
Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser	
130 135 140	
ttc gtt ggc gca ttt ctg gtt gtc gga tct tca ttt atc ttg ccc tat	480
Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr	
145 150 155 160	
tta cgt cgg gtt att acg cct acc gtc agc ggt att gtg gta ctg atg	528
Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met	
165 170 175	
atc ggc tta agc ctg att aaa gtc ggc att atc gat ttt ggt gga gga	576
Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly	
180 185 190	
ttt gca gcc aaa agc agc ggt acg ttc ggc aat tac gaa cat ctc ggc	624
Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly	
195 200 205	
gtt ggt tta ttg gtt tta att gtg gtg atc ggc ttt aac tgc tgt cgc	672

Arg	Leu	Ser	Ala	Tyr	Glu	Ala	Phe	Tyr	Leu	Ala	Thr	Leu	Gly	Gly	Ala	
	355						360					365				
aaa	tct	ctg	ggc	ctt	gac	gat	ttg	att	ggc	aac	ttt	tta	cct	ggc	aaa	1152
Lys	Ser	Leu	Gly	Leu	Asp	Asp	Leu	Ile	Gly	Asn	Phe	Leu	Pro	Gly	Lys	
	370					375				380						
gag	gct	gat	ttc	gtg	gtg	atg	gaa	ccc	acc	gcc	act	ccg	cta	cag	cag	1200
Glu	Ala	Asp	Phe	Val	Val	Met	Glu	Pro	Thr	Ala	Thr	Pro	Leu	Gln	Gln	
	385				390					395					400	
ctg	cgc	tat	gac	aac	tct	gtt	tct	tta	gtc	gac	aaa	ttg	ttc	gtg	atg	1248
Leu	Arg	Tyr	Asp	Asn	Ser	Val	Ser	Leu	Val	Asp	Lys	Leu	Phe	Val	Met	
				405					410					415		
atg	acg	ttg	ggc	gat	gac	cgt	tcg	atc	tac	cgc	acc	tac	gtt	gat	ggc	1296
Met	Thr	Leu	Gly	Asp	Asp	Arg	Ser	Ile	Tyr	Arg	Thr	Tyr	Val	Asp	Gly	
			420					425					430			
cgt	ctg	gtg	tac	gaa	cgc	aac	taa									1320
Arg	Leu	Val	Tyr	Glu	Arg	Asn	*									
		435														

<210> 108
 <211> 570
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(570)

<400>	108															
atg	tct	gga	gac	atc	cta	caa	aca	ccg	gac	gca	cca	aag	cca	cag	ggc	48
Met	Ser	Gly	Asp	Ile	Leu	Gln	Thr	Pro	Asp	Ala	Pro	Lys	Pro	Gln	Gly	
	1				5				10					15		
gcg	ctg	gat	aat	tat	ttt	aaa	att	acc	gct	cgt	ggc	agt	acc	gtt	cgt	96
Ala	Leu	Asp	Asn	Tyr	Phe	Lys	Ile	Thr	Ala	Arg	Gly	Ser	Thr	Val	Arg	
			20					25					30			
cag	gaa	gta	ctg	gct	ggc	tta	acg	acc	ttt	ctg	gcc	atg	gtt	tat	tcc	144
Gln	Glu	Val	Leu	Ala	Gly	Leu	Thr	Thr	Phe	Leu	Ala	Met	Val	Tyr	Ser	
		35					40					45				
gtt	atc	gtc	gtt	ccg	gga	atg	ctg	ggc	aaa	gca	ggt	ttt	cct	ccc	gca	192
Val	Ile	Val	Val	Pro	Gly	Met	Leu	Gly	Lys	Ala	Gly	Phe	Pro	Pro	Ala	
	50					55					60					
gct	gtg	ttt	gtt	gcc	acc	tgt	ctg	gtc	gcg	ggc	ttc	ggc	tcg	ttg	ctg	240
Ala	Val	Phe	Val	Ala	Thr	Cys	Leu	Val	Ala	Gly	Phe	Gly	Ser	Leu	Leu	
	65				70				75						80	
atg	gga	tta	tgg	gct	aat	ttg	cca	atg	gcg	att	ggt	tgc	gcg	att	tcc	288
Met	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Met	Ala	Ile	Gly	Cys	Ala	Ile	Ser	
				85					90					95		

ttg acg gcg ttt acc gca ttc agt ctg gta ctc ggg caa caa att agc	336
Leu Thr Ala Phe Thr Ala Phe Ser Leu Val Leu Gly Gln Gln Ile Ser	
100 105 110	

gtt cct gtc gca ctg ggc gcg gta ttt ctg atg ggc gtc atc ttc acc	384
Val Pro Val Ala Leu Gly Ala Val Phe Leu Met Gly Val Ile Phe Thr	
115 120 125	

gcc att tcc gta acc ggt gtg cgt acc tgg atc tta cgt aat ttg ccg	432
Ala Ile Ser Val Thr Gly Val Arg Thr Trp Ile Leu Arg Asn Leu Pro	
130 135 140	

atg ggt atc gct cac ggt aca ggt atc ggt atc ggg ctg ttt ctg ctg	480
Met Gly Ile Ala His Gly Thr Gly Ile Gly Ile Gly Leu Phe Leu Leu	
145 150 155 160	

ctg att gct gct aac ggt gtg ggt atg gtt atc aaa aac ccg att gaa	528
Leu Ile Ala Ala Asn Gly Val Gly Met Val Ile Lys Asn Pro Ile Glu	
165 170 175	

ggc ttg cag tgg cgc tcg gtg cgt tta cct cct tcc cgg tga	570
Gly Leu Gln Trp Arg Ser Val Arg Leu Pro Pro Ser Arg *	
180 185	

<210> 109
 <211> 831
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(831)

<400> 109	
gtg gcg ctc ggt gcg ttt acc tcc ttc ccg gtg atg atg agc ttg ctg	48
Met Ala Leu Gly Ala Phe Thr Ser Phe Pro Val Met Met Ser Leu Leu	
1 5 10 15	

ggg ctg gcg gtc atc ttc ggc ctg gag aag tgt cgc gta ccc ggc ggg	96
Gly Leu Ala Val Ile Phe Gly Leu Glu Lys Cys Arg Val Pro Gly Gly	
20 25 30	

atc ttg ttg gtg att att gca att tcg atc atc ggc tta atc ttt gac	144
Ile Leu Leu Val Ile Ile Ala Ile Ser Ile Ile Gly Leu Ile Phe Asp	
35 40 45	

cca gcg gtg aaa tac cac ggt ctg gtg gcg atg cca agc ctg act ggc	192
Pro Ala Val Lys Tyr His Gly Leu Val Ala Met Pro Ser Leu Thr Gly	
50 55 60	

gaa gat ggt aag tct ctg att ttc agc ctc gat att atg ggt gca ctc	240
Glu Asp Gly Lys Ser Leu Ile Phe Ser Leu Asp Ile Met Gly Ala Leu	
65 70 75 80	

cag cca act gta ctt ccg agt gta ctg gca ttg gtg atg acc gca gtg	288
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val	
85 90 95	
ttc gac gct act ggc acc atc cgt gcc gtc gcc ggt cag gcg aat ttg	336
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu	
100 105 110	
ttg gat aaa gac aac cag atc atc aac ggc ggc aaa gcc ctg acc agt	384
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser	
115 120 125	
gac tca gta agt tca ata ttc tcc ggc ctg gtg ggc gca gcg ccc gca	432
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala	
130 135 140	
gcg gtt tat atc gaa tca gcg gca gga acc gcc gcc ggg ggt aaa aca	480
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr	
145 150 155 160	
ggg tta acc gca acc gta gtg ggg gcg tta ttc ctg tta att ctg ttt	528
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe	
165 170 175	
tta tca ccg ctg tca ttt ttg atc cct ggt tac gcc act gca ccc gct	576
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala	
180 185 190	
ctg atg tac gta ggt ttg ctg atg tta agt aac gtc tcg aag ctg gat	624
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp	
195 200 205	
ttc aat gat ttt att gac gct atg gct ggc ctg gtg tgt gcc gtg ttc	672
Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe	
210 215 220	
atc gtt ctg act tgt aat atc gtt acc ggt att atg ctg ggc ttt gtg	720
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val	
225 230 235 240	
aca ctg gtc gta ggc cgc gtc ttt gca cgc gaa tgg caa aag ctg aat	768
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn	
245 250 255	
att ggt acg gtg atc att act gcc gca ctg gtc gca ttt tac gcg ggt	816
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly	
260 265 270	
ggg tgg gca atc taa	831
Gly Trp Ala Ile *	
275	

<210> 110

<211> 1401

<212> DNA

<213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1401)

<400> 110

atg aat agc gaa ggg ggg aaa ccg ggg aat gta ctg acc gtt aac ggc	48
Met Asn Ser Glu Gly Gly Lys Pro Gly Asn Val Leu Thr Val Asn Gly	
1 5 10 15	
aac tat acc gga aac aat ggc ctg atg acg ttc aac gcg acg ctg ggc	96
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly	
20 25 30	
ggc gat aat tcg ccc acc gat aag atg aac gtg aaa ggc gat acc caa	144
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln	
35 40 45	
ggg aac act cgc gtt cgg gtt gat aac att ggc ggc gtc ggt gca caa	192
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln	
50 55 60	
acg gtc aac ggt att gaa ctc att gag gtt ggc ggt aat tct gca ggt	240
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly	
65 70 75 80	
aac ttc gcg ctg acc acc gga act gtc gaa gct ggg gct tac gtc tac	288
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr	
85 90 95	
acg ctg gct aaa ggg aag ggg aat gac gag aaa aac tgg tat ctg acc	336
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr	
100 105 110	
agt aaa tgg gac ggc gta acg cca gcg gat aca ccc gat ccc atc aat	384
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn	
115 120 125	
aat ccc cct gtt gtg gat ccg gaa ggc cca tca gtt tat cgc ccg gag	432
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu	
130 135 140	
gcc gga agc tat atc agc aac att gcc gca gcc aac tcg ctg ttt agc	480
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Ala Asn Ser Leu Phe Ser	
145 150 155 160	
cat cgt tta cac gac cgt ctg ggt gag ccg cag tat aca gat tca ctg	528
His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu	
165 170 175	
cat tct cag ggg tcg gca agc agt atg tgg atg cgt cat gtc gga ggg	576
His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly	
180 185 190	
cac gaa cgt tca agg gcc ggt gac ggt cag cta aat act cag gct aac	624
His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn	
195 200 205	

aaa gta aat aac aac ctt agc ctg tgg ggg aat gtc ggt gtg caa cta 1344
 Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
 435 440 445

ggt gat aaa ggc tat agc gat act cag ggc atg ctg gga gtg aaa tat 1392
 Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
 450 455 460

agc tgg taa 1401
 Ser Trp *
 465

<210> 111
 <211> 3978
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3978)

<400> 111
 atg aat aga atc tat cgc gtg ata tgg aat tgc act cta cag gta ttt 48
 Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
 1 5 10 15

cag gcc tgc tgc gaa tta act cgc agg gca ggt aaa aca tgc acg gtt 96
 Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
 20 25 30

aat ttg cgt aaa tcc tct gga ctg aca acg aaa ttc agt aga ttg acg 144
 Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
 35 40 45

ctg ggt gtt ttg ctg gca cta agc ggt tca gcg tct ggt gca agt ctg 192
 Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
 50 55 60

gaa gtt gat aat gat cag att acc aat att gat act gat gtt gct tat 240
 Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
 65 70 75 80

gat gcc tac ctg gtt ggc tgg tat ggc act gga gtg ctt aat att ttg 288
 Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
 85 90 95

gct ggc ggt aat gcc tcc tta acc act att act acc agc gtc att ggc 336
 Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly
 100 105 110

gct aat gag gac tca gag ggc acc gtt aat gtt ttg ggt ggc acc tgg 384
 Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp
 115 120 125

cga ttg tat gat agc gga aat aat gca agg cct tta aat gtg ggt caa 432
 Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln

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1045	1050	1055	
gat ggt gca ctt ggc aac acc cgg gaa ctg aac atc agc aac gcg gcc			3216
Asp Gly Ala Leu Gly Asn Thr Arg Glu Leu Asn Ile Ser Asn Ala Ala			
1060	1065	1070	
atc gtc gat ctt aat gga tgc acg cag acg gta gag aca ttc acc ggg			3264
Ile Val Asp Leu Asn Gly Ser Thr Gln Thr Val Glu Thr Phe Thr Gly			
1075	1080	1085	
cag atg ggt tgc act gtt ttg ttc aaa gag ggg gcg ctg acg gta aat			3312
Gln Met Gly Ser Thr Val Leu Phe Lys Glu Gly Ala Leu Thr Val Asn			
1090	1095	1100	
aaa ggt ggg atc agt cag ggt gaa ctg aca ggt ggc gga aac ctg aat			3360
Lys Gly Gly Ile Ser Gln Gly Glu Leu Thr Gly Gly Gly Asn Leu Asn			
1105	1110	1115	1120
gtt aca ggg gga acg ctg gct atc gag ggg ctt aat gca cgc tac aat			3408
Val Thr Gly Gly Thr Leu Ala Ile Glu Gly Leu Asn Ala Arg Tyr Asn			
1125	1130	1135	
gcg tta acc agc att agc cca aat gcg gaa gtc agc ctc gat aat act			3456
Ala Leu Thr Ser Ile Ser Pro Asn Ala Glu Val Ser Leu Asp Asn Thr			
1140	1145	1150	
cag ggg tta ggc aga gga aat att gcc aat gac ggt ctg tta acg cta			3504
Gln Gly Leu Gly Arg Gly Asn Ile Ala Asn Asp Gly Leu Leu Thr Leu			
1155	1160	1165	
aaa aac gtg act ggc gaa ctg cgt aat agc ata agc ggg aag ggt atc			3552
Lys Asn Val Thr Gly Glu Leu Arg Asn Ser Ile Ser Gly Lys Gly Ile			
1170	1175	1180	
gtg agc gca acc gcc agg aca gat gta gag ttg gat ggc gat aat agc			3600
Val Ser Ala Thr Ala Arg Thr Asp Val Glu Leu Asp Gly Asp Asn Ser			
1185	1190	1195	1200
cgc ttt gtg ggg caa ttc aac att gat aca ggc agc gcg ctc agc gtc			3648
Arg Phe Val Gly Gln Phe Asn Ile Asp Thr Gly Ser Ala Leu Ser Val			
1205	1210	1215	
aac gag cag aaa aac ctg ggt gat gct tcc gtt atc aat aat ggc ctg			3696
Asn Glu Gln Lys Asn Leu Gly Asp Ala Ser Val Ile Asn Asn Gly Leu			
1220	1225	1230	
ctc acc atc tcc act gag cgt agc tgg gcg atg acg cac agt atc agc			3744
Leu Thr Ile Ser Thr Glu Arg Ser Trp Ala Met Thr His Ser Ile Ser			
1235	1240	1245	
ggt agc ggt gat gtg aca aaa ctg ggt acc ggg atc ctg act ctt aac			3792
Gly Ser Gly Asp Val Thr Lys Leu Gly Thr Gly Ile Leu Thr Leu Asn			
1250	1255	1260	
aac gat tcc gcg gcg tat cag ggt acg acg gat atc gtg ggg ggg gaa			3840
Asn Asp Ser Ala Ala Tyr Gln Gly Thr Thr Asp Ile Val Gly Gly Glu			
1265	1270	1275	1280

att gct ttc ggt tcc gac tct gcc att aat atg gca agt caa cac att	3888
Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile	
1285 1290 1295	
aat atc cat aac agc ggt gtg atg tcg gga aat gtc acc act gca ggt	3936
Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly	
1300 1305 1310	
gat atg aac gtt atg cct ggg ggg ggc act gcg tgt cgc taa	3978
Asp Met Asn Val Met Pro Gly Gly Gly Thr Ala Cys Arg *	
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<210> 112
 <211> 756
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(756)

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1 5 10 15	
ttg ggc ttt gtg acc gtt gag aaa gtc gtt gag cgt ctg gga att tcg	96
Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser	
20 25 30	
cct gcc act gcg cga cgc gat atc aat aaa ctt gac gaa agc ggc aaa	144
Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys	
35 40 45	
ctg aaa aaa gtg cgc aat ggc gca gaa gct att acc caa cag cgc ccg	192
Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro	
50 55 60	
cgc tgg acg ccg atg aat ctg cat cag gcg cag aat cac gat gaa aaa	240
Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys	
65 70 75 80	
gta cgt atc gct aaa gcg gcc tcg cag ctg gtt aat ccg ggc gaa agc	288
Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser	
85 90 95	
gta gtc atc aac tgc ggc tcc acc gcg ttt ctg ctt ggg cgg gaa atg	336
Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met	
100 105 110	
tgt ggc aag cca gtg caa atc atc act aat tat cta ccg ctg gca aat	384
Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn	
115 120 125	

000123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899

007466-1400

tac ctg atc gat caa gaa cat gac agc gtg atc att atg ggc gga cag 432
Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln
130 135 140

tac aac aaa agt cag tcc atc act tta agc ccg cag ggc agc gaa aac 480
Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn
145 150 155 160

agt ctc tat gcc ggg cac tgg atg ttt acc agc gga aaa ggg ctg acc 528
Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr
165 170 175

gca gaa ggg ttg tat aaa acc gat atg ctg aca gca atg gca gag cag 576
Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln
180 185 190

aag atg ctg agc gtg gta ggg aaa ctg gtg gta ctg gtt gat agc agt 624
Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser
195 200 205

aag att ggc gaa cgc gcg gga atg ctt ttt agc cgt gcc gat caa atc 672
Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile
210 215 220

gat atg ctt atc acc ggc aaa aat gct aac ccg gaa atc ctg caa caa 720
Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln
225 230 235 240

ctg gaa gcg caa ggg gtc agc att ctg cgt gtt taa 756
Leu Glu Ala Gln Gly Val Ser Ile Leu Arg Val *

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<211> 825

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(825)

<400> 113

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1 5 10 15

atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg 96
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
20 25 30

cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc 144
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
35 40 45

att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc 192
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr

<210> 114
 <211> 519
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(519)

<400> 114
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 1 5 10 15
 gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc 96
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 act aac aaa ata tcg ctt gtc agt tat att gta tgg cag gaa aga tat 144
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 gcg act gat att aca gat ccc caa agt gga gag ttt atg acc att aaa 192
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
 50 55 60
 aat aag atg ttg ctg ggt gcg ctt ttg ctg gtt acc agt gcc gcc tgg 240
 Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
 65 70 75 80
 gcc gca cca gcc acc gcg ggt tcg acc aat acc tcg gga att tct aag 288
 Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
 85 90 95
 tat gag tta agt agt ttc att gct gac ttt aag cat ttc aaa cca ggg 336
 Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
 100 105 110
 gac acc gta cca gaa atg tac cgt acc gat gag tac aac att aag cag 384
 Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
 115 120 125
 tgg cag ttg cgt aac ctg ccc gcg cct gat gcc ggg acg cac tgg acc 432
 Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
 130 135 140
 tat atg ggt ggc gcg tac gtg ttg atc agc gac acc gac ggt aaa atc 480
 Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
 145 150 155 160
 att aaa gcc tac gac ggt gag att ttt tat cat cgc taa 519
 Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg *
 165 170

[illegible]

51

Gly	Ile	Glu	Ala	Tyr	Ala	Ala	Glu	Glu	Thr	Phe	Asp	Thr	His	Phe	Met		
			20				25						30				
ata	ggg	gga	atg	aaa	gac	cag	cag	gtt	gca	aat	att	cgt	ctt	gat	gat	144	
Ile	Gly	Gly	Met	Lys	Asp	Gln	Gln	Val	Ala	Asn	Ile	Arg	Leu	Asp	Asp		
			35				40						45				
aat	caa	ccc	tta	ccg	ggg	cag	tat	gac	atc	gat	att	tat	gtc	aat	aag	192	
Asn	Gln	Pro	Leu	Pro	Gly	Gln	Tyr	Asp	Ile	Asp	Ile	Tyr	Val	Asn	Lys		
			50				55						60				
caa	tgg	cgc	ggg	aaa	tat	gag	att	att	gtt	aaa	gac	aac	ccg	caa	gaa	240	
Gln	Trp	Arg	Gly	Lys	Tyr	Glu	Ile	Ile	Val	Lys	Asp	Asn	Pro	Gln	Glu		
			65				70						75	80			
aca	tgt	tta	tca	aga	gaa	gtt	atc	aag	cgg	tta	ggc	att	aat	agc	gat	288	
Thr	Cys	Leu	Ser	Arg	Glu	Val	Ile	Lys	Arg	Leu	Gly	Ile	Asn	Ser	Asp		
			85						90						95		
aac	ttc	gcc	agc	ggg	aag	caa	tgt	tta	aca	ttt	gag	caa	ctt	gtt	cag	336	
Asn	Phe	Ala	Ser	Gly	Lys	Gln	Cys	Leu	Thr	Phe	Glu	Gln	Leu	Val	Gln		
			100						105						110		
ggg	ggg	agc	tat	acc	tgg	gat	atc	ggg	gtt	ttt	cgt	ctc	gat	ttc	agt	384	
Gly	Gly	Ser	Tyr	Thr	Trp	Asp	Ile	Gly	Val	Phe	Arg	Leu	Asp	Phe	Ser		
			115						120						125		
gtc	ccg	cag	gcc	tgg	gtg	gaa	gaa	ctg	gaa	agt	ggc	tat	gtt	cca	ccg	432	
Val	Pro	Gln	Ala	Trp	Val	Glu	Glu	Leu	Glu	Ser	Gly	Tyr	Val	Pro	Pro		
			130						135						140		
gaa	aac	tgg	gag	cgg	ggg	att	aat	gcg	ttt	tat	acc	tct	tat	tat	ctg	480	
Glu	Asn	Trp	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Tyr	Thr	Ser	Tyr	Tyr	Leu		
			145			150			155						160		
agt	cag	tat	tac	agc	gac	tat	aaa	gcg	tcg	ggg	aat	aac	aag	agt	aca	528	
Ser	Gln	Tyr	Tyr	Ser	Asp	Tyr	Lys	Ala	Ser	Gly	Asn	Asn	Lys	Ser	Thr		
			165						170						175		
tat	gta	cgt	ttt	aac	agc	ggg	tta	aat	tta	ctg	ggg	tgg	caa	ctg	cat	576	
Tyr	Val	Arg	Phe	Asn	Ser	Gly	Leu	Asn	Leu	Leu	Gly	Trp	Gln	Leu	His		
			180						185						190		
tct	gat	gcc	agt	ttc	agt	aaa	aca	aat	aac	aat	cca	ggg	gtg	tgg	aaa	624	
Ser	Asp	Ala	Ser	Phe	Ser	Lys	Thr	Asn	Asn	Asn	Pro	Gly	Val	Trp	Lys		
			195			200						205					
agc	aat	acc	ctg	tat	ctg	gaa	cgt	gga	ttt	gcc	caa	ctt	ctc	ggc	acg	672	
Ser	Asn	Thr	Leu	Tyr	Leu	Glu	Arg	Gly	Phe	Ala	Gln	Leu	Leu	Gly	Thr		
			210			215			220								
ctt	cgc	gtg	ggg	gat	atg	tac	aca	tca	agc	gat	att	ttt	gat	tct	gtt	720	
Leu	Arg	Val	Gly	Asp	Met	Tyr	Thr	Ser	Ser	Asp	Ile	Phe	Asp	Ser	Val		
			225			230			235						240		
cgc	ttc	agag	ggg	gtg	cgg	ttg	ttt	cgt	gat	atg	cag	atg	ttg	cct	aac	768	
Arg	Phe	Arg	Gly	Val	Arg	Leu	Phe	Arg	Asp	Met	Gln	Met	Leu	Pro	Asn		

				245				250				255							
tcg	aaa	caa	aat	ttt	acg	cca	cgg	gtg	cag	ggg	att	gct	cag	agt	aac	816			
Ser	Lys	Gln	Asn	Phe	Thr	Pro	Arg	Val	Gln	Gly	Ile	Ala	Gln	Ser	Asn				
				260				265				270							
gcg	ctg	gta	act	att	gaa	cag	aat	ggg	ttt	gtg	gtt	tat	cag	aaa	gag	864			
Ala	Leu	Val	Thr	Ile	Glu	Gln	Asn	Gly	Phe	Val	Val	Tyr	Gln	Lys	Glu				
				275				280				285							
gtt	cct	cct	ggc	ccg	ttc	gcg	att	aca	gat	ttg	cag	ttg	gcc	ggg	ggg	912			
Val	Pro	Pro	Gly	Pro	Phe	Ala	Ile	Thr	Asp	Leu	Gln	Leu	Ala	Gly	Gly				
				290				295				300							
gga	gca	gat	ctt	gat	gtc	agc	gtg	aaa	gag	gcg	gac	ggc	tcg	gta	acc	960			
Gly	Ala	Asp	Leu	Asp	Val	Ser	Val	Lys	Glu	Ala	Asp	Gly	Ser	Val	Thr				
				310				315				320							
acc	tat	ctg	gtg	cct	tat	gca	gcg	gtg	cca	aat	atg	ctg	caa	ccc	ggc	1008			
Thr	Tyr	Leu	Val	Pro	Tyr	Ala	Ala	Val	Pro	Asn	Met	Leu	Gln	Pro	Gly				
				325				330				335							
gtg	tcg	aaa	tat	gat	tta	gcg	gcg	ggg	cgt	agc	cat	att	gaa	ggg	gcg	1056			
Val	Ser	Lys	Tyr	Asp	Leu	Ala	Ala	Gly	Arg	Ser	His	Ile	Glu	Gly	Ala				
				340				345				350							
agc	aaa	caa	agt	gat	ttt	gtc	cag	gcg	ggg	tat	cag	tat	ggg	ttt	aat	1104			
Ser	Lys	Gln	Ser	Asp	Phe	Val	Gln	Ala	Gly	Tyr	Gln	Tyr	Gly	Phe	Asn				
				355				360				365							
aat	tta	ttg	acg	ctg	tat	ggg	ggc	tcg	atg	gtc	gcg	aat	aat	tat	tac	1152			
Asn	Leu	Leu	Thr	Leu	Tyr	Gly	Gly	Ser	Met	Val	Ala	Asn	Asn	Tyr	Tyr				
				370				375				380							
gcg	ttt	act	ttg	ggg	gct	ggc	tgg	aat	aca	cgc	att	ggg	gcc	att	tcc	1200			
Ala	Phe	Thr	Leu	Gly	Ala	Gly	Trp	Asn	Thr	Arg	Ile	Gly	Ala	Ile	Ser				
				385				390				395				400			
gtc	gat	gcc	act	aag	tcg	cat	agt	aaa	caa	gac	aac	ggc	gat	gtg	ttt	1248			
Val	Asp	Ala	Thr	Lys	Ser	His	Ser	Lys	Gln	Asp	Asn	Gly	Asp	Val	Phe				
				405				410				415							
gac	ggg	caa	agt	tat	caa	att	gcc	tac	aac	aaa	ttt	gtg	agc	caa	acg	1296			
Asp	Gly	Gln	Ser	Tyr	Gln	Ile	Ala	Tyr	Asn	Lys	Phe	Val	Ser	Gln	Thr				
				420				425				430							
tcg	acg	cgt	ttt	ggg	ctg	gcg	gcc	tgg	cgt	tat	tcg	tcg	cgt	gat	tac	1344			
Ser	Thr	Arg	Phe	Gly	Leu	Ala	Ala	Trp	Arg	Tyr	Ser	Ser	Arg	Asp	Tyr				
				435				440				445							
cgg	aca	ttt	aac	gat	cac	gtt	tgg	gca	aac	aat	aaa	gat	aat	tat	cgc	1392			
Arg	Thr	Phe	Asn	Asp	His	Val	Trp	Ala	Asn	Asn	Lys	Asp	Asn	Tyr	Arg				
				450				455				460							
cgt	gat	gaa	aac	gat	gtc	tat	gac	att	gcc	gat	tat	tac	cag	aac	gat	1440			
Arg	Asp	Glu	Asn	Asp	Val	Tyr	Asp	Ile	Ala	Asp	Tyr	Tyr	Gln	Asn	Asp				
				465				470				475				480			

50	55	60	
ctg cag gcg tgg att gat gat ggc gat acg tca tta cca cca gaa aaa			240
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys			
65	70	75	80
att cag gtt cct ttc atg tta acg cca cca gtg gca aaa ata ggg gca			288
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala			
	85	90	95
aat tcc ggg cag caa gta aaa atc aaa att atg ccg aat aaa ctg ccc			336
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro			
	100	105	110
act aat aaa gaa agc att ttt tat ctg aat gtt ctg gat att cca cca			384
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro			
	115	120	125
aat agt cca gag caa gaa ggt aag aat gca ctg aag ttt gcg atg caa			432
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln			
	130	135	140
aac aga att aag ttg ttt tac cgg cca gcg ggt att gct ccg gta aat			480
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn			
	145	150	155
aaa gcg aca ttt aaa aaa ttg ctg gta aat cgc agt ggc aat ggt ttg			528
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu			
	165	170	175
gtg ata aaa aat gac tca gct aat tgg gtg acg att tcg gat gtc aaa			576
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys			
	180	185	190
gct aat aat gtc aaa gtc aat tat gaa act att atg att gcc ccc tta			624
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu			
	195	200	205
gaa agt cag agt gtt aat gtc aaa agt aat aat gca aat aac tgg cat			672
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His			
	210	215	220
ctg acc att atc gat gac cat ggc aac tat att agt gac aaa att taa			720
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile *			
	225	230	235

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 <211> 543
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(543)

[illegible]

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<210> 119
<211> 288
<212> DNA
<213> Escherichia coli
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58

<222> (1)...(288)

<400> 119

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Met	Leu	His	Thr	Leu	His	Arg	Ser	Pro	Trp	Leu	Thr	Asp	Phe	Ala	Ala	
1				5				10						15		

ctg	ctg	cgt	ctg	ctc	agt	gaa	gga	gac	gaa	ctg	cta	tta	ttg	caa	gat	96
Leu	Leu	Arg	Leu	Leu	Ser	Glu	Gly	Asp	Glu	Leu	Leu	Leu	Leu	Gln	Asp	
			20					25					30			

ggc	gta	act	gcc	gca	gtt	gac	ggt	aac	cgc	tac	ctt	gaa	agt	ctg	cgt	144
Gly	Val	Thr	Ala	Ala	Val	Asp	Gly	Asn	Arg	Tyr	Leu	Glu	Ser	Leu	Arg	
		35					40					45				

aat	gcc	ccc	att	aag	gtc	tat	gcc	ctg	aac	gaa	gac	ctt	att	gcc	cgc	192
Asn	Ala	Pro	Ile	Lys	Val	Tyr	Ala	Leu	Asn	Glu	Asp	Leu	Ile	Ala	Arg	
	50					55					60					

ggt	ttg	act	ggt	caa	att	tcg	aac	gac	atc	att	ctc	att	gac	tat	act	240
Gly	Leu	Thr	Gly	Gln	Ile	Ser	Asn	Asp	Ile	Ile	Leu	Ile	Asp	Tyr	Thr	
65					70				75						80	

gat	ttc	gtc	aga	ctt	acg	gtt	aag	cac	ccc	agc	cag	atg	gcc	tgg	tga	288
Asp	Phe	Val	Arg	Leu	Thr	Val	Lys	His	Pro	Ser	Gln	Met	Ala	Trp	*	
				85					90					95		

<210> 120

<211> 360

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(360)

<400> 120

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Met	Lys	Arg	Ile	Ala	Phe	Val	Phe	Ser	Thr	Ala	Pro	His	Gly	Thr	Ala	
1				5				10					15			

gca	ggc	cgg	gaa	ggt	tta	gat	gct	tta	ctg	gca	act	tcc	gca	tta	act	96
Ala	Gly	Arg	Glu	Gly	Leu	Asp	Ala	Leu	Leu	Ala	Thr	Ser	Ala	Leu	Thr	
			20					25					30			

gac	gat	ctg	gct	gtc	ttc	ttt	ata	gct	gat	ggc	gtt	ttt	cag	ctg	ctg	144
Asp	Asp	Leu	Ala	Val	Phe	Phe	Ile	Ala	Asp	Gly	Val	Phe	Gln	Leu	Leu	
		35					40					45				

cca	gga	caa	aag	ccc	gat	gca	gtg	ctg	gcg	cgt	gat	tac	att	gcc	act	192
Pro	Gly	Gln	Lys	Pro	Asp	Ala	Val	Leu	Ala	Arg	Asp	Tyr	Ile	Ala	Thr	
	50					55					60					

ttt	aaa	ttg	ttg	ggt	ctg	tac	gac	att	gaa	cag	tgc	tgg	gtt	tgt	gcg	240
Phe	Lys	Leu	Leu	Gly	Leu	Tyr	Asp	Ile	Glu	Gln	Cys	Trp	Val	Cys	Ala	

[illegible]

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<220>  
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[illegible]

tga
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387

<210> 122
<211> 735
<212> DNA
<213> Escherichia coli

<220>
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<400> 122

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1				5				10						15		
ttg	gat	tta	ctg	gat	caa	cgt	cct	ttc	gac	cag	acc	gat	ttt	gat	att	96
Leu	Asp	Leu	Leu	Asp	Gln	Arg	Pro	Phe	Asp	Gln	Thr	Asp	Phe	Asp	Ile	
			20					25						30		
ctg	aaa	tcc	tac	gaa	gcg	gtg	gtg	gac	ggg	tta	gcg	atg	ctt	att	ggc	144
Leu	Lys	Ser	Tyr	Glu	Ala	Val	Val	Asp	Gly	Leu	Ala	Met	Leu	Ile	Gly	
		35					40					45				
tcc	cac	tgt	gaa	atc	gtt	ttg	cac	tct	ttg	cag	gat	cta	aaa	tgt	tca	192
Ser	His	Cys	Glu	Ile	Val	Leu	His	Ser	Leu	Gln	Asp	Leu	Lys	Cys	Ser	
	50					55				60						
gcc	att	cgc	att	gct	aac	ggg	gaa	cat	aca	ggc	cgg	aag	att	ggg	tcg	240
Ala	Ile	Arg	Ile	Ala	Asn	Gly	Glu	His	Thr	Gly	Arg	Lys	Ile	Gly	Ser	
65					70				75					80		
cca	att	act	gac	ctg	gcg	cta	cgt	atg	ctg	cac	gat	atg	acg	gga	gcg	288
Pro	Ile	Thr	Asp	Leu	Ala	Leu	Arg	Met	Leu	His	Asp	Met	Thr	Gly	Ala	
				85					90					95		
gat	agc	agc	gtt	tct	aaa	tgc	tac	ttt	act	cgc	gcc	aaa	agc	ggc	gta	336
Asp	Ser	Ser	Val	Ser	Lys	Cys	Tyr	Phe	Thr	Arg	Ala	Lys	Ser	Gly	Val	
			100					105						110		
tta	atg	aag	tcc	ctg	act	atc	gcg	att	cgt	aac	cgc	gaa	cag	cgt	gta	384
Leu	Met	Lys	Ser	Leu	Thr	Ile	Ala	Ile	Arg	Asn	Arg	Glu	Gln	Arg	Val	
		115					120					125				
att	ggg	ctg	ctg	tgc	atc	aat	atg	aat	ctt	gat	gtt	ccc	ttc	tcg	cag	432
Ile	Gly	Leu	Leu	Cys	Ile	Asn	Met	Asn	Leu	Asp	Val	Pro	Phe	Ser	Gln	
	130					135				140						
att	atg	agc	acc	ttt	gtg	ccg	cca	gaa	acc	ccg	gat	gtc	ggg	tca	agc	480
Ile	Met	Ser	Thr	Phe	Val	Pro	Pro	Glu	Thr	Pro	Asp	Val	Gly	Ser	Ser	
145					150					155				160		
gtc	aac	ttt	gcc	tct	tct	gtt	gaa	gat	ctg	gtt	acc	caa	acg	ctg	gag	528
Val	Asn	Phe	Ala	Ser	Ser	Val	Glu	Asp	Leu	Val	Thr	Gln	Thr	Leu	Glu	

<210> 124
 <211> 192
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(192)

<400> 124
 atg aaa gca aaa gag ctg cgt gag aag agc gtt gaa gag ctg aac acc 48
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 gag ctg ctg aac ctg ctg cgt gag cag ttc aac ctg cgt atg cag gct 96
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 gca agt ggc cag ctg caa cag tct cac ctg ttg aag caa gtg cgt cgc 144
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 gat gtc gca cgc gtt aag act tta ctg aac gag aag gcg ggt gcg taa 192
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala *
 50 55 60

<210> 125
 <211> 411
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(411)

<400> 125
 atg tta caa cca aag cgt aca aaa ttc cgt aaa atg cac aaa ggc cgt 48
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 aac cgc ggt ctg gcg cag ggt acg gat gtt agc ttc ggc agc ttc ggt 96
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 ctg aaa gct gtt ggc cgt ggt cgt ctg act gcc cgt cag atc gaa gca 144
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 gca cgt cgt gct atg acc cgt gca gtt aag cgt caa ggt aag atc tgg 192
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 atc cgt gtg ttc ccg gac aaa ccg atc act gaa aag ccg ctg gca gtg 240
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val

50	55	60	
gac att gac gat ctg aaa gtt acg aaa att ttc gta gac gaa ggc ccg			240
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro			
65	70	75	80
agc atg aag cgc att atg ccg cgt gca aaa ggt cgt gca gat cgc atc			288
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile			
85	90		95
ctg aag cgc acc agc cac atc act gtg gtt gtg tcc gat cgc tga			333
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg *			
100	105		110

<210> 128
 <211> 279
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(279)

<400>	128	
atg cca cgt tct ctc aag aaa ggt cct ttt att gac ctg cac ttg ctg		48
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu		
1	5	10
aag aag gta gag aaa gcg gtg gaa agc gga gac aag aag ccc ctg cgc		96
Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg		
20	25	30
act tgg tcc cgt cgt tca acg atc ttt cct aac atg atc ggt ttg acc		144
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr		
35	40	45
atc gct gtc cat aat ggt cgt cag cac gtt ccg gta ttt gta acc gac		192
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp		
50	55	60
gaa atg gtt ggt cac aaa ctg ggt gaa ttc gca ccg act cgt act tat		240
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr		
65	70	75
cgc ggc cac gct gct gat aaa aaa gcg aag aag aaa taa		279
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys *		
85	90	

<210> 129
 <211> 822
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS
 <222> (1)...(822)

<400> 129

atg gca gtt gtt aaa tgt aaa ccg aca tct ccg ggt cgt cgc cac gta	48
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val	
1 5 10 15	
gtt aaa gtg gtt aac cct gag ctg cac aag ggc aaa cct ttt gct ccg	96
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro	
20 25 30	
ttg ctg gaa aaa aac agc aaa tcc ggt ggt cgt aac aac aat ggc cgt	144
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg	
35 40 45	
atc acc act cgt cat atc ggt ggt ggc cac aag cag gct tac cgt att	192
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile	
50 55 60	
gtt gac ttc aaa cgc aac aaa gac ggt atc ccg gca gtt gtt gaa cgt	240
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg	
65 70 75 80	
ctt gag tac gat ccg aac cgt tcc gcg aac atc gcg ctg gtt ctg tac	288
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr	
85 90 95	
aaa gac ggt gaa cgc cgt tac atc ctg gcc cct aaa ggc ctg aaa gct	336
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala	
100 105 110	
ggc gac cag att cag tct ggc gtt gat gct gca atc aaa cca ggt aac	384
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn	
115 120 125	
acc ctg ccg atg cgc aac atc ccg gtt ggt tct act gtt cat aac gta	432
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val	
130 135 140	
gaa atg aaa cca ggt aaa ggc ggt cag ctg gca cgt tcc gct ggt act	480
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr	
145 150 155 160	
tac gtt cag atc gtt gct cgt gat ggt gct tat gtc acc ctg cgt ctg	528
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu	
165 170 175	
cgt tct ggt gaa atg cgt aaa gta gaa gca gac tgc cgt gca act ctg	576
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu	
180 185 190	
ggc gaa gtt ggc aat gct gag cat atg ctg cgc gtt ctg ggt aaa gca	624
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala	
195 200 205	
ggg gct gca cgc tgg cgt ggt gtt cgt ccg acc gtt cgc ggt acc gcg	672

<210> 131
 <211> 606
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(606)

<400> 131

atg gaa tta gta ttg aaa gac gcg cag agc gcg ctg act gtt tcc gaa	48
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu	
1 5 10 15	
act acc ttc ggt cgt gat ttc aac gaa gcg ctg gtt cac cag gtt gtt	96
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val	
20 25 30	
gtt gct tat gca gct ggt gct cgt cag ggt act cgt gct cag aag act	144
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr	
35 40 45	
cgt gct gaa gta act ggt tcc ggt aaa aaa ccg tgg cgc cag aaa ggc	192
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly	
50 55 60	
acc ggc cgt gcg cgt tct ggt tct atc aag agc ccg atc tgg cgt tct	240
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser	
65 70 75 80	
ggt ggc gtg acc ttt gct gct cgt ccg cag gac cac agt caa aaa gtt	288
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val	
85 90 95	
aac aag aag atg tac cgc ggc gcg ctg aaa agc atc ctg tcc gaa ctg	336
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu	
100 105 110	
gta cgt cag gat cgt ctg atc gtt gtc gag aag ttc tct gta gaa gcg	384
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala	
115 120 125	
ccg aaa act aag ctg ctg gca cag aaa ctg aaa gac atg gct ctg gaa	432
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu	
130 135 140	
gat gtg ctg atc atc acc ggt gag ctg gac gaa aac ctg ttc ctg gct	480
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala	
145 150 155 160	
gcg cgc aac ctg cac aag gtt gac gta cgc gat gca act ggt atc gac	528
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp	
165 170 175	
ccg gtt agc ctg atc gcc ttc gac aaa gtc gta atg act gct gat gct	576

Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190

gtt aag caa gtt gag gag atg ctg gca tga 606
 Val Lys Gln Val Glu Glu Met Leu Ala *
 195 200

<210> 132
 <211> 630
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(630)

<400> 132
 atg att ggt tta gtc ggt aaa aaa gtg ggt atg acc cgt atc ttc aca 48
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15

gaa gac ggc gtt tct atc cca gta acc gta atc gaa gtt gaa gca aac 96
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30

cgc gtt act cag gtt aaa gac ctg gct aac gat ggc tac cgt gct att 144
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45

cag gtg acc acc ggt gct aaa aaa gct aac cgt gtg acc aag cct gaa 192
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60

gct ggc cac ttc gct aaa gct ggc gta gaa gct ggc cgt ggt ctg tgg 240
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80

gaa ttc cgc ctg gct gaa ggc gaa gag ttc act gta ggt cag agc att 288
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95

agc gtt gaa ctg ttt gct gac gtt aaa aaa gtt gac gta act ggc acc 336
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110

tct aaa ggt aaa ggt ttc gca ggt acc gtt aag cgc tgg aac ttc cgt 384
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125

acc cag gac gct act cac ggt aac tcc ttg tct cac cgc gtt ccg ggt 432
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140

tct atc ggt cag aac cag act ccg ggc aaa gtg ttc aaa ggc aag aaa 480
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160

atg gca ggt cag atg ggt aac gaa cgt gta acc gtt cag agc ctt gac	528
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp	
165 170 175	
gta gta cgc gtt gac gct gag cgc aac ctg ctg ctg gtt aaa ggt gct	576
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala	
180 185 190	
gtc ccg ggt gca acc ggt agc gac ctg atc gtt aaa cca gct gtg aag	624
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys	
195 200 205	
gcg taa	630
Ala *	

<210> 133
 <211> 312
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(312)

<400> 133	
atg cag aac caa aga atc cgt atc cgc ctg aaa gcg ttt gat cat cgt	48
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg	
1 5 10 15	
ctg atc gat caa gca acc gcg gaa atc gtc gag act gcc aag cgc act	96
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr	
20 25 30	
ggt gcg cag gtc cgt ggt ccg atc ccg ctg ccg aca cgc aaa gag cgc	144
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg	
35 40 45	
ttc act gtt ctg atc tcc ccg cac gtc aac aaa gac gcg cgc gat cag	192
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln	
50 55 60	
tac gaa atc cgt act cac ttg cgt ctg gtt gac atc gtt gag cca acc	240
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr	
65 70 75 80	
gag aaa acc gtt gat gct ctg atg cgt ctg gat ctg gct gcc ggt gta	288
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val	
85 90 95	
gac gtg cag atc agc ctg ggt taa	312
Asp Val Gln Ile Ser Leu Gly *	
100	

<210> 134
 <211> 315
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(315)

<400> 134
 atg atc cgc aaa gcc ttt gtc atg cag gta aac ccc gac gcc cac gaa 48
 Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
 1 5 10 15
 gag tat cag cgt cgg cat aat ccc atc tgg cca gaa ctg gaa gca gtg 96
 Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
 20 25 30
 ctg aaa tct cac ggt gcg cat aac tac gcc atc tat ctc gac aaa gcg 144
 Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
 35 40 45
 cgt aat ctg ctg ttt gcc atg gta gag att gaa tct gaa gaa cgc tgg 192
 Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
 50 55 60
 aat gcg gtt gcc agc act gat gtt tgc caa cgt tgg tgg aaa tat atg 240
 Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
 65 70 75 80
 acc gat gtt atg ccc gct aac ccg gat aac agc ccg gtg agt agc gag 288
 Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
 85 90 95
 ctg caa gaa gtg ttt tac ctg ccg taa 315
 Leu Gln Glu Val Phe Tyr Leu Pro *

<210> 135
 <211> 864
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(864)

<400> 135
 atg atc cgc agt atg acc gcc tac gcc cgg cgt gaa atc aag ggt gaa 48
 Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
 1 5 10 15
 tgg ggg agc gca acc tgg gaa atg cgc tcg gta aac cag cgt tat ctg 96
 Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
 20 25 30

Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
 260 265 270

aaa gtg ttg att gag cag atg cgc gag cag att cag aac atc gaa taa 864
 Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu *
 275 280 285

<210> 136
 <211> 492
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(492)

<400> 136
 atg agc aca gaa aca att gaa ata ttc aat aat agt gat gaa tgg gca 48
 Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
 1 5 10 15
 aat caa cta aaa cac gca tta tcg aaa gga gaa aat ctg gca tta cta 96
 Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
 20 25 30
 cat ggt tta act cct gat atc ctt gat aga ata tat gca tat gca ttc 144
 His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
 35 40 45
 gac tac cat gaa aag ggt aat ata acg gac gca gaa att tat tat aaa 192
 Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
 50 55 60
 ttc ttg tgc att tat gcg ttc gaa aat cat gag tat cta aaa gat ttt 240
 Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
 65 70 75 80
 gca tca gta tgt cag ccc aaa aag aaa tat caa caa gca tat gac ctt 288
 Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
 85 90 95
 tac aaa cta agt tac aat tac ttc ccg tat gat gac tat tca gtt att 336
 Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
 100 105 110
 tat cgt atg ggt caa tgt cag att ggg gct aaa aat atc gat aac gca 384
 Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
 115 120 125
 atg caa tgt ttc tat cac att att aac aat tgt gag gat gat agt gtt 432
 Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
 130 135 140
 aag agt aaa gcg cag gca tat att gaa ctc tta aac gat aat tca gaa 480
 Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu

145 150 155 160

gat aat ggc taa 492
Asp Asn Gly *

<210> 137
<211> 1947
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1947)

<400> 137
atg aat att tta ggt ttt ttc cag cga ctc ggt agg gcg tta cag ctc 48
Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
1 5 10 15
cct atc gcg gtg ctg ccg gtg gcg gca ctg ttg ctg cga ttc ggt cag 96
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
20 25 30
cca gat tta ctt aac gtt gcg ttt att gcc cag gcg ggc ggt gcg att 144
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
35 40 45
ttt gat aac ctc gca tta atc ttc gcc atc ggt gtg gca tcc agc tgg 192
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
50 55 60
tcg aaa gac agc gct ggt gcg gcg gcg ctg gcg ggt gcg gta ggt tac 240
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
65 70 75 80
ttt gtg tta acc aaa gcg atg gtg acc atc aac cca gaa att aac atg 288
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
85 90 95
ggt gta ctg gcg ggt atc att acc ggt ctg gtt ggt ggc gca gcc tat 336
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
100 105 110
aac cgt tgg tcc gat att aaa ctg ccg gac ttc ctg agc ttc ttc ggc 384
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
115 120 125
ggc aaa cgc ttt gtg ccg att gcc acc gga ttc ttc tgc ctg gtg ctg 432
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
130 135 140
gcg gcc att ttt ggt tac gtc tgg ccg ccg gta cag cac gct atc cat 480
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
145 150 155 160

610

615

620

ttc agt ggc ttg atc att aaa gct cag ggc cat att gtg gcg ggt caa 1920
 Phe Ser Gly Leu Ile Ile Lys Ala Gln Gly His Ile Val Ala Gly Gln
 625 630 635 640

aca ccg ctg tat gaa atc aaa aag taa 1947
 Thr Pro Leu Tyr Glu Ile Lys Lys *
 645

<210> 138

<211> 1239

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1239)

<400> 138

atg aag act atc ttc agg tac att ctt ttt tta gca ctg tat tct tgt 48
 Met Lys Thr Ile Phe Arg Tyr Ile Leu Phe Leu Ala Leu Tyr Ser Cys
 1 5 10 15

tgt aat aca gtc agt gca tat aca agt ttt att gtg gga aat aat gca 96
 Cys Asn Thr Val Ser Ala Tyr Thr Ser Phe Ile Val Gly Asn Asn Ala
 20 25 30

gga gtt gat aac tat cga ggc ccc tcc act gcc gca cag atg acc ttt 144
 Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
 35 40 45

aat tac aca tca aca gca agc aac ttg gtt ttt tat aaa ccc acg cag 192
 Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
 50 55 60

ctc ggc ccg act ggg gta aaa atg tac tgg tca tac ctg gat aca ggt 240
 Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
 65 70 75 80

acc ggt ggt ggt att ctt tac tgc aat aca tct ggc aga gcg aat cct 288
 Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
 85 90 95

ggt cca ata act att gaa aat gcc atg gtc tat tca ggt aaa gat tat 336
 Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
 100 105 110

ggc gga cat aaa cta ttt aat aca tct gtt cct ggt ctg tat tac acc 384
 Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
 115 120 125

atg tta ata tca agg gtc tgg tct gca tac gat aca ata act gac att 432
 Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
 130 135 140

caa Gln 145	tcg Ser	cca Pro	gga Gly	atc Ile	tat Tyr 150	atc Ile	gga Gly	gat Asp	cct Pro	tcc Ser 155	aac Asn	caa Gln	gaa Glu	ttt Phe	ttc Phe 160	480
ttt Phe	tcc Ser	gtc Val	aca Thr	gac Asp 165	agc Ser	gat Asp	cta Leu	caa Gln	act Thr 170	aag Lys	ggt Gly	tgc Cys	aac Asn	aaa Lys 175	gca Ala	528
gac Asp	gac Asp	tac Tyr	gat Asp 180	aag Lys	ttt Phe	tgg Trp	gct Ala	att Ile 185	ggt Gly	ggt Gly	ata Ile	gta Val	cac His 190	aac Asn	ata Ile	576
act Thr	gtt Val	gaa Glu 195	ttt Phe	tat Tyr	aca Thr	gat Asp	act Thr 200	aat Asn	ttc Phe	gat Asp	cct Pro	aca Thr 205	ctt Leu	aat Asn	cag Gln	624
caa Gln 210	gtc Val	cag Gln	tta Leu	tcc Ser	agt Ser	tca Ser 215	tca Ser	aat Asn	tac Tyr	ctt Leu 220	tat Tyr	tcg Ser	ttt Phe	aag Lys	gcc Ala	672
tac Tyr 225	agt Ser	cct Pro	ggt Gly	aca Thr	aaa Lys 230	gtt Val	gta Val	gat Asp	cac His	agc Ser 235	aac Asn	cac His	att Ile	tat Tyr	gtc Val 240	720
aat Asn	ttc Phe	aca Thr	ctg Leu	aat Asn 245	aat Asn	gtc Val	aaa Lys	tta Leu	acc Thr 250	tta Leu	cca Pro	aca Thr	tgt Cys	ttt Phe 255	acc Thr	768
tcc Ser	ata Ile	ctt Leu	acc Thr 260	ggg Gly	cca Pro	tca Ser	gtc Val	aat Asn 265	ggt Gly	tca Ser	acg Thr	gtt Val	aga Arg 270	atg Met	gga Gly	816
gaa Glu	tat Tyr	agc Ser 275	tct Ser	ggg Gly	aca Thr	att Ile	aaa Lys 280	aat Asn	ggc Gly	gct Ala	tca Ser	cct Pro 285	gtt Val	ccc Pro	ttt Phe	864
gat Asp 290	atc Ile	tcg Ser	ctt Leu	cag Gln	aat Asn	tgt Cys 295	att Ile	cgt Arg	gtg Val	cgt Arg	aat Asn 300	att Ile	gaa Glu	aca Thr	aaa Lys	912
ctc Leu 305	gtc Val	act Thr	gga Gly	aaa Lys	gta Val 310	ggg Gly	act Thr	caa Gln	aac Asn	aca Thr 315	caa Gln	ctg Leu	ctt Leu	ggg Gly	aat Asn 320	960
acg Thr	ctt Leu	act Thr	gga Gly	agc Ser 325	act Thr	gcc Ala	gcc Ala	aaa Lys	ggc Gly 330	gtt Val	ggc Gly	gta Val	ctc Leu	att Ile 335	gaa Glu	1008
ggg Gly 340	tta Leu	gca Ala	acc Thr	agt Ser	aaa Lys	aat Asn	ccg Pro	cta Leu 345	atg Met	aca Thr	tta Leu	aaa Lys	cct Pro 350	aat Asn	gat Asp	1056
acg Thr	aat Asn	tct Ser 355	gtt Val	tat Tyr	ata Ile	gat Asp	tat Tyr 360	gaa Glu	acc Thr	gaa Glu	gat Asp 365	gac Thr	acc Thr	tcc Ser	gat Asp	1104
ggg	gtt	tac	cct	aat	caa	ggt	aac	ggc	aca	tca	caq	cct	ctt	cat	ttc	1152

Gly	Val	Tyr	Pro	Asn	Gln	Gly	Asn	Gly	Thr	Ser	Gln	Pro	Leu	His	Phe		
370						375					380						
cag	gca	aca	tta	aag	caa	gac	ggg	aat	att	gct	atc	gaa	ccc	ggc	gaa	1200	
Gln	Ala	Thr	Leu	Lys	Gln	Asp	Gly	Asn	Ile	Ala	Ile	Glu	Pro	Gly	Glu		
385					390					395					400		
ttt	aaa	gcc	acc	agt	act	ttc	cag	gta	acc	tat	ccc	tga				1239	
Phe	Lys	Ala	Thr	Ser	Thr	Phe	Gln	Val	Thr	Tyr	Pro	*					
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Met	His	Pro	Thr	Gln	Arg	Lys	Leu	Met	Lys	Arg	Ile	Ile	Leu	Phe	Leu		
1				5				10					15				
tca	tta	ctg	ttt	tgc	atc	gcc	tgt	cca	gcc	att	gct	gga	cag	gat	att	96	
Ser	Leu	Leu	Phe	Cys	Ile	Ala	Cys	Pro	Ala	Ile	Ala	Gly	Gln	Asp	Ile		
			20					25					30				
gac	ctt	gtt	gcc	aat	gta	aaa	aac	agc	acc	tgc	aaa	agc	gga	atc	agt	144	
Asp	Leu	Val	Ala	Asn	Val	Lys	Asn	Ser	Thr	Cys	Lys	Ser	Gly	Ile	Ser		
		35				40						45					
aac	cag	ggt	aat	att	gat	ctt	ggc	gtc	gtt	ggg	gtg	gga	tat	ttt	tca	192	
Asn	Gln	Gly	Asn	Ile	Asp	Leu	Gly	Val	Val	Gly	Val	Gly	Tyr	Phe	Ser		
	50					55					60						
ggt	aat	gtt	act	cct	gaa	agt	tat	caa	cca	ggt	gga	aaa	gag	ttc	act	240	
Gly	Asn	Val	Thr	Pro	Glu	Ser	Tyr	Gln	Pro	Gly	Gly	Lys	Glu	Phe	Thr		
65				70				75						80			
atc	act	gta	tcc	gac	tgt	gca	tta	cag	gga	act	ggc	gat	gtg	cta	aat	288	
Ile	Thr	Val	Ser	Asp	Cys	Ala	Leu	Gln	Gly	Thr	Gly	Asp	Val	Leu	Asn		
			85					90						95			
cag	tta	cat	att	gat	ttt	aga	gcc	ctt	agc	ggt	gtc	atg	gct	gct	ggc	336	
Gln	Leu	His	Ile	Asp	Phe	Arg	Ala	Leu	Ser	Gly	Val	Met	Ala	Ala	Gly		
			100					105					110				
tct	agg	caa	ata	ttt	gct	aat	gaa	att	tcg	tca	gga	gca	agt	aat	gta	384	
Ser	Arg	Gln	Ile	Phe	Ala	Asn	Glu	Ile	Ser	Ser	Gly	Ala	Ser	Asn	Val		
		115				120						125					
gga	gta	gtt	ata	ttt	tct	act	cag	gat	tcg	gcg	aat	aca	ttc	aat	gtt	432	
Gly	Val	Val	Ile	Phe	Ser	Thr	Gln	Asp	Ser	Ala	Asn	Thr	Phe	Asn	Val		
	130					135					140						

Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val	
115 120 125	
gcc gtt gaa gtc tgg agc act gta act ccg gca aca ggg agt gca aca	432
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr	
130 135 140	
caa ttt agc tgt gta aca cca gca tca caa gag gta aca atc tcc act	480
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr	
145 150 155 160	
gca gcc aat gcg gtc gtt tat tat ccg atg agt gca cgc ctg gtc gtg	528
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val	
165 170 175	
gaa aaa aat aaa acc gta aac aat gtc act gcg ggt aag ttt tct gca	576
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala	
180 185 190	
cca gcc aca ttt aca gta acc tat aac taa	606
Pro Ala Thr Phe Thr Val Thr Tyr Asn *	
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1 5 10 15	
aaa aca acg cca cat aaa ata gtg ata ctg atg gga ata tta tta tca	96
Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser	
20 25 30	
ccc tca gta ttt gca acg gat att aat gta gag ttt aca gcc act gtc	144
Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val	
35 40 45	
aaa gcg aca acc tgt aac atc aca ctt act ggt aat aac gtc acg aat	192
Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn	
50 55 60	
gat ggc aat aat aac tac aca ttg aga atc cct aag atg ggt ctg gat	240
Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp	
65 70 75 80	
aag atc gcg aat aaa acg aca gaa tct cag gct gat ttt aaa ctg gtt	288
Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val	
85 90 95	

Leu	Ser	Gly	Gly	Ile	Leu	Glu	Val	Gln	Pro	Gly	Asn	Val	Thr	Val	Leu	
65					70					75					80	
gcc	gac	acc	gca	att	cgc	ggc	cag	gat	ctc	gac	gaa	gcg	cga	gcc	atg	288
Ala	Asp	Thr	Ala	Ile	Arg	Gly	Gln	Asp	Leu	Asp	Glu	Ala	Arg	Ala	Met	
				85				90						95		
gaa	gcg	aaa	cgt	aag	gct	gaa	gag	cac	att	agc	agc	tct	cac	ggc	gac	336
Glu	Ala	Lys	Arg	Lys	Ala	Glu	Glu	His	Ile	Ser	Ser	Ser	His	Gly	Asp	
			100					105					110			
gta	gat	tac	gct	cag	gcg	tct	gcg	gaa	ctg	gcc	aaa	gcg	atc	gcg	cag	384
Val	Asp	Tyr	Ala	Gln	Ala	Ser	Ala	Glu	Leu	Ala	Lys	Ala	Ile	Ala	Gln	
		115					120					125				
ctg	cgc	ggt	atc	gag	ttg	acc	aaa	aaa	gcg	atg	taa					420
Leu	Arg	Val	Ile	Glu	Leu	Thr	Lys	Lys	Ala	Met	*					
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Met	Ala	Thr	Gly	Lys	Ile	Val	Gln	Val	Ile	Gly	Ala	Val	Val	Asp	Val	
1				5				10						15		
gaa	ttc	cct	cag	gat	gcc	gta	ccg	cgc	gtg	tac	gat	gct	ctt	gag	gtg	96
Glu	Phe	Pro	Gln	Asp	Ala	Val	Pro	Arg	Val	Tyr	Asp	Ala	Leu	Glu	Val	
			20					25					30			
caa	aat	ggt	aat	gag	cgt	ctg	gtg	ctg	gaa	gtt	cag	cag	cag	ctc	ggc	144
Gln	Asn	Gly	Asn	Glu	Arg	Leu	Val	Leu	Glu	Val	Gln	Gln	Gln	Leu	Gly	
		35				40					45					
ggc	ggt	atc	gta	cgt	acc	atc	gca	atg	ggt	tcc	tcc	gac	ggt	ctg	cgt	192
Gly	Gly	Ile	Val	Arg	Thr	Ile	Ala	Met	Gly	Ser	Ser	Asp	Gly	Leu	Arg	
	50					55					60					
cgc	ggt	ctg	gat	gta	aaa	gac	ctc	gaa	cac	ccg	att	gaa	gtc	ccg	gta	240
Arg	Gly	Leu	Asp	Val	Lys	Asp	Leu	Glu	His	Pro	Ile	Glu	Val	Pro	Val	
65					70				75					80		
ggt	aaa	gcg	act	ctg	ggc	cgt	atc	atg	aac	gta	ctg	ggt	gaa	ccg	gtc	288
Gly	Lys	Ala	Thr	Leu	Gly	Arg	Ile	Met	Asn	Val	Leu	Gly	Glu	Pro	Val	
				85				90					95			
gac	atg	aaa	ggc	gag	atc	ggt	gaa	gaa	gag	cgt	tgg	gcg	att	cac	cgc	336
Asp	Met	Lys	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Arg	Trp	Ala	Ile	His	Arg	
			100				105						110			

gca gca cct tcc tac gaa gag ctg tca aac tct cag gaa ctg ctg gaa	384
Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu	
115 120 125	
acc ggt atc aaa gtt atc gac ctg atg tgt ccg ttc gct aag ggc ggt	432
Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly	
130 135 140	
aaa gtt ggt ctg ttc ggt ggt gcg ggt gta ggt aaa acc gta aac atg	480
Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met	
145 150 155 160	
atg gag ctc att cgt aac atc gcg atc gag cac tcc ggt tac tct gtg	528
Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val	
165 170 175	
ttt gcg ggc gta ggt gaa cgt act cgt gag ggt aac gac ttc tac cac	576
Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His	
180 185 190	
gaa atg acc gac tcc aac gtt atc gac aaa gta tcc ctg gtg tat ggc	624
Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly	
195 200 205	
cag atg aac gag ccg ccg gga aac cgt ctg cgc gtt gct ctg acc ggt	672
Gln Met Asn Glu Pro Pro Gly Asn Arg Leu Arg Val Ala Leu Thr Gly	
210 215 220	
ctg acc atg gct gag aaa ttc cgt gac gaa ggt cgt gac gtt ctg ctg	720
Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu	
225 230 235 240	
ttc gtt gac aac atc tat cgt tac acc ctg gcc ggt acg gaa gta tcc	768
Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser	
245 250 255	
gca ctg ctg ggc cgt atg cct tca gcg gta ggt tat cag ccg acc ctg	816
Ala Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu	
260 265 270	
gcg gaa gag atg ggc gtt ctg cag gaa cgt atc acc tcc acc aaa act	864
Ala Glu Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Thr	
275 280 285	
ggt tct atc acc tcc gta cag gca gta tac gta cct gcg gat gac ttg	912
Gly Ser Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu	
290 295 300	
act gac ccg tct ccg gca acc acc ttt gcg cac ctt gac gca acc gtg	960
Thr Asp Pro Ser Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Val	
305 310 315 320	
gta ctg agc cgt cag atc gcg tct ctg ggt atc tac ccg gcc gtt gac	1008
Val Leu Ser Arg Gln Ile Ala Ser Leu Gly Ile Tyr Pro Ala Val Asp	
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 <213> Escherichia coli

<220>
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 <222> (1)...(1542)

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gct cag ttc aat gtt gtg agt gaa gct cac aac gaa ggt act att gtt 96
 Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
 20 25 30

tct gta agt gac ggt gtt atc cgc att cac ggc ctg gcc gat tgt atg 144
 Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
 35 40 45

cag ggt gaa atg atc tcc ctg ccg ggt aac cgt tac gct atc gca ctg 192
 Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
 50 55 60

aac ctc gag cgc gac tct gta ggt gcg gtt gtt atg ggt ccg tac gct 240
 Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
 65 70 75 80

gac ctt gcc gaa ggc atg aaa gtt aag tgt act ggc cgt atc ctg gaa 288
 Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
 85 90 95

gtt ccg gtt ggc cgt ggc ctg ctg ggc cgt gtg gtt aac act ctg ggt 336
 Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
 100 105 110

gca cca atc gac ggt aaa ggt ccg ctg gat cac gac ggc ttc tct gct 384
 Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
 115 120 125

gta gaa gca atc gct ccg ggc gtt atc gaa cgt cag tcc gta gat cag 432
 Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln
 130 135 140

ccg gta cag acc ggt tat aaa gcc gtt gac tcc atg atc cca atc ggt 480
 Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly
 145 150 155 160

cgt ggt cag cgt gaa ttg atc atc ggt gac cgt cag aca ggt aaa acc 528
 Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
 165 170 175

gca ctg gct atc gat gcc atc atc aac cag cgc gat tcc ggt atc aaa	576
Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys	
180 185 190	
tgt atc tat gtc gct atc ggc cag aaa gcg tcc acc att tct aac gtg	624
Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val	
195 200 205	
gta cgt aaa ctg gaa gag cac ggc gca ctg gct aac acc atc gtt gtg	672
Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val	
210 215 220	
gta gca acc gcg tct gaa tcc gct gca ctg caa tac ctg gca ccg tat	720
Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr	
225 230 235 240	
gcc ggt tgc gca atg ggc gaa tac ttc cgt gac cgc ggt gaa gat gcg	768
Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala	
245 250 255	
ctg atc att tac gat gac ctg tct aaa cag gct gtt gct tac cgt cag	816
Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln	
260 265 270	
atc tcc ctg ctg ctc cgt cgt ccg cca gga cgt gaa gca ttc ccg ggc	864
Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly	
275 280 285	
gac gtt ttc tac ctc cac tct cgt ctg ctg gag cgt gct gca cgt gtt	912
Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val	
290 295 300	
aac gcc gaa tac gtt gaa gcc ttc acc aaa ggt gaa gtg aaa ggg aaa	960
Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys	
305 310 315 320	
acc ggt tct ctg acc gca ctg ccg att atc gaa act cag gcg ggt gac	1008
Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp	
325 330 335	
gtt tct gcg ttc gtt ccg acc aac gta atc tcc att acc gat ggt cag	1056
Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln	
340 345 350	
atc ttc ctg gaa acc aac ctg ttc aac gcc ggt att cgt cct gcg gtt	1104
Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val	
355 360 365	
aac ccg ggt att tcc gta tcc cgt gtt ggt ggt gca gca cag acc aag	1152
Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys	
370 375 380	
atc atg aaa aaa ctg tcc ggt ggt atc cgt acc gct ctg gca cag tat	1200
Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr	
385 390 395 400	
cgt gaa ctg gca gcg ttc tct cag ttt gca tcc gac ctt gac gat gca	1248

Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala	
405 410 415	
aca cgt aag cag ctt gac cac ggt cag aaa gtg acc gaa ctg ctg aaa	1296
Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys	
420 425 430	
cag aaa cag tat gcg ccg atg tcc gtt gcg cag cag tct ctg gtt ctg	1344
Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu	
435 440 445	
ttc gca gca gaa cgt ggt tac ctg gcg gat gtt gaa ctg tcg aaa att	1392
Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile	
450 455 460	
ggc agc ttc gaa gcc gct ctg ctg gct tac gtc gac cgt gat cac gct	1440
Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala	
465 470 475 480	
ccg ttg atg caa gag atc aac cag acc ggt ggc tac aac gac gaa atc	1488
Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile	
485 490 495	
gaa ggc aag ctg aaa ggc atc ctc gat tcc ttc aaa gca acc caa tcc	1536
Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser	
500 505 510	
tggttaa	1542
Trp *	

<210> 146
 <211> 534
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(534)

<400> 146	
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Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe	
1 5 10 15	
gac ttt gcc gtc gaa cac caa agt gta gaa cgc tgg cag gac atg ctg	96
Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu	
20 25 30	
gcg ttt gcc gcc gag gta acc aaa aac gaa caa atg gca gag ctt ctc	144
Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu	
35 40 45	
tct ggc gcg ctt gcg cca gaa acg ctc gcc gag tcg ttt atc gca gtt	192
Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val	
50 55 60	

tgt ggt gag caa ctg gac gaa aac ggt cag aac ctg att cgg gtt atg	240
Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met	
65 70 75 80	

gct gaa aat ggt cgt ctt aac gcg ctc ccg gat gtt ctg gag cag ttt	288
Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe	
85 90 95	

att cac ctg cgt gcc gtg agt gag gct acc gct gag gta gac gtc att	336
Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile	
100 105 110	

tcc gct gcc gca ctg agt gaa caa cag ctc gcg aaa att tct gct gcg	384
Ser Ala Ala Ala Leu Ser Glu Gln Gln Leu Ala Lys Ile Ser Ala Ala	
115 120 125	

atg gaa aaa cgt ctg tca cgc aaa gtt aag ctg aat tgc aaa atc gat	432
Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp	
130 135 140	

aag tct gta atg gca ggc gtt atc atc cga gcg ggt gat atg gtc att	480
Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile	
145 150 155 160	

gat ggc agc gta cgc ggt cgt ctt gag cgc ctt gca gac gtc ttg cag	528
Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln	
165 170 175	

tct taa	534
Ser *	

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 <211> 471
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(471)

<400> 147	
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1 5 10 15	

ttc gtt ctg ttc tgc atg aag tac gta tgg ccg cca tta atg gca gcc	96
Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala	
20 25 30	

atc gaa aaa cgt caa aaa gaa att gct gac ggc ctt gct tcc gca gaa	144
Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu	
35 40 45	

cga gca cat aag gac ctt gac ctt gca aag gcc agc gcg acc gac cag	192
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<210> 149
 <211> 816
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(816)

<400> 149
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 Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
 1 5 10 15
 aat aac ctt cag ctg gac ctg cgt aca ttc tcg ctg gtg gat cca caa 96
 Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
 20 25 30
 aac ccc cca gcc acc ttc tgg aca atc aat att gac tcc atg ttc ttc 144
 Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
 35 40 45
 tcg gtg gtg ctg ggt ctg ttg ttc ctg gtt tta ttc cgt agc gta gcc 192
 Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
 50 55 60
 aaa aag gcg acc agc ggt gtg cca ggt aag ttt cag acc gcg att gag 240
 Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
 65 70 75 80
 ctg gtg atc ggc ttt gtt aat ggt agc gtg aaa gac atg tac cat ggc 288
 Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
 85 90 95
 aaa agc aag ctg att gct ccg ctg gcc ctg acg atc ttc gtc tgg gta 336
 Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
 100 105 110
 ttc ctg atg aac ctg atg gat tta ctg cct atc gac ctg ctg ccg tac 384
 Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
 115 120 125
 att gct gaa cat gta ctg ggt ctg cct gca ctg cgt gtg gtt ccg tct 432
 Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
 130 135 140
 gcg gac gtg aac gta acg ctg tct atg gca ctg ggc gta ttt atc ctg 480
 Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
 145 150 155 160
 att ctg ttc tac agc atc aaa atg aaa ggc atc ggc ggc ttc acg aaa 528
 Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
 165 170 175

gag ttg acg ctg cag ccg ttc aat cac tgg gcg ttc att cct gtc aac	576
Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn	
180 185 190	
tta atc ctt gaa ggg gta agc ctg ctg tcc aaa cca gtt tca ctc ggt	624
Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly	
195 200 205	
ttg cga ctg ttc ggt aac atg tat gcc ggt gag ctg att ttc att ctg	672
Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu	
210 215 220	
att gct ggt ctg ttg ccg tgg tgg tca cag tgg atc ctg aat gtg ccg	720
Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro	
225 230 235 240	
tgg gcc att ttc cac atc ctg atc att acg ctg caa gcc ttc atc ttc	768
Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe	
245 250 255	
atg gtt ctg acg atc gtc tat ctg tgc atg gcg tct gaa gaa cat taa	816
Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His *	
260 265 270	
<210> 150	
<211> 393	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(393)	
<400> 150	
gtg aaa aac gtg atg tct gtg tgc ctc gtg agt cga aac gtt gct ccg	48
Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg	
1 5 10 15	
aag ctt ctg ctc gtt cag tta ctg gtg gtg ata gca agt gga ttg ctg	96
Lys Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu	
20 25 30	
ttc agc ctc aaa gac ccc ttc tgg ggc gtc tct gca ata agc ggg ggc	144
Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly	
35 40 45	
ctg gca gtc ttt ctg cct aac gtt ttg ttt atg ata ttt gcc tgg cgt	192
Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg	
50 55 60	
cac cag gcg cat aca cca gcg aaa ggc cgg gtg gcc tgg aca ttc gca	240
His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala	
65 70 75 80	
ttt ggc gaa gct ttc aaa gtt ctg gcg atg ttg gtg tta ctg gtg gtg	288

Phe Gly Glu Ala	Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val	
	85 90 95	
gcg ttg gcg gtt tta aag gcg gta ttc ttg ccg ctg atc gtt acg tgg	336	
Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp		
	100 105 110	
gtt ttg gtg ctg gtg gtt cag ata ctg gca ccg gct gta att aac aac	384	
Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn		
	115 120 125	
aaa ggg taa	393	
Lys Gly *		
	130	

<210> 151
 <211> 1242
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1242)

<400> 151	
atg caa aaa cac ggc gac cgc tat gtg tgg atc aac ccg cct gct att	48
Met Gln Lys His Gly Asp Arg Tyr Val Trp Ile Asn Pro Pro Ala Ile	
1 5 10 15	
ccg ctt tct acc gaa gag atg gac agc gtt ttt gcg ctg cca tac aag	96
Pro Leu Ser Thr Glu Glu Met Asp Ser Val Phe Ala Leu Pro Tyr Lys	
	20 25 30
cgc gtg cca cat ccg gcc tat ggc aat gcc cgt att ccg gct tac gaa	144
Arg Val Pro His Pro Ala Tyr Gly Asn Ala Arg Ile Pro Ala Tyr Glu	
	35 40 45
atg atc cgt ttt tcg gtc aac att atg cgt ggc tgc ttt ggc ggc tgc	192
Met Ile Arg Phe Ser Val Asn Ile Met Arg Gly Cys Phe Gly Gly Cys	
	50 55 60
tct ttc tgt tct atc acc gag cac gaa ggg cgc att att cag agc cgt	240
Ser Phe Cys Ser Ile Thr Glu His Glu Gly Arg Ile Ile Gln Ser Arg	
	65 70 75 80
tcc gaa gat tcg atc att aat gag atc gaa gcg atc cgc gac acc gtt	288
Ser Glu Asp Ser Ile Ile Asn Glu Ile Glu Ala Ile Arg Asp Thr Val	
	85 90 95
cca ggt ttt acg ggc gtg att tcc gat ctt ggt ggg cca act gcc aac	336
Pro Gly Phe Thr Gly Val Ile Ser Asp Leu Gly Gly Pro Thr Ala Asn	
	100 105 110
atg tat atg ttg cgc tgc aaa tcg cca cgc gct gaa caa act tgt cgc	384
Met Tyr Met Leu Arg Cys Lys Ser Pro Arg Ala Glu Gln Thr Cys Arg	
	115 120 125

cca acc att gaa gag atg cgt gaa gct cgt cgc cag aac cgc aat acc	1104
Pro Thr Ile Glu Glu Met Arg Glu Ala Arg Arg Gln Asn Arg Asn Thr	
355 360 365	
cgt ccg gcg ttg acg aaa cat acg ccg atg gcg acc cag cgt cag acg	1152
Arg Pro Ala Leu Thr Lys His Thr Pro Met Ala Thr Gln Arg Gln Thr	
370 375 380	
cct gct acg gca aaa aaa gcg tcg tct acg caa tct cgt ccg gtg aat	1200
Pro Ala Thr Ala Lys Lys Ala Ser Ser Thr Gln Ser Arg Pro Val Asn	
385 390 395 400	
gct ggt gcg aag aaa cgg cct aaa gcg gcg gtt gga cgt taa	1242
Ala Gly Ala Lys Lys Arg Pro Lys Ala Ala Val Gly Arg *	
405 410	

<210> 152
 <211> 978
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(978)

<400> 152	
atg agc tct atc tcc ctg atc caa ccg gat cgc gac ctg ttc tcc tgg	48
Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp	
1 5 10 15	
ccg cag tac tgg gcc gcc tgt ttt gga ccg gca ccg ttt ttg ccg atg	96
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met	
20 25 30	
tct cgt gaa gag atg gat caa ctt ggc tgg gat agc tgc gac atc att	144
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile	
35 40 45	
ttg gtt act ggc gac gcg tat gtc gat cac cca agc ttc ggg atg gcg	192
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala	
50 55 60	
att tgc ggt cgt atg ctg gaa gcg cag ggc ttt cgc gtc ggg atc atc	240
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile	
65 70 75 80	
gcc cag ccg gac tgg agc agc aaa gac gac ttt atg cgt ctg ggt aaa	288
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys	
85 90 95	
ccg aat ctg ttt ttc ggt gtt act gct ggc aac atg gat tcg atg atc	336
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile	
100 105 110	
aac cgt tat acc gcc gat cgc cgt tta cgt cat gac gat gcc tac acg	384

Asn	Arg	Tyr	Thr	Ala	Asp	Arg	Arg	Leu	Arg	His	Asp	Asp	Ala	Tyr	Thr		
		115					120					125					
ccg	gat	aac	gtc	gcg	ggt	aag	cgc	ccg	gat	cgc	gcc	aca	ctg	ggt	tat	432	
Pro	Asp	Asn	Val	Ala	Gly	Lys	Arg	Pro	Asp	Arg	Ala	Thr	Leu	Val	Tyr		
		130				135					140						
acc	cag	cgt	tgt	aaa	gag	gcg	tgg	aaa	gat	gta	ccg	gtg	atc	ctc	ggc	480	
Thr	Gln	Arg	Cys	Lys	Glu	Ala	Trp	Lys	Asp	Val	Pro	Val	Ile	Leu	Gly		
		145			150					155					160		
ggt	att	gag	gct	agt	ctg	cgc	cgt	acc	gcg	cat	tat	gat	tac	tgg	tcc	528	
Gly	Ile	Glu	Ala	Ser	Leu	Arg	Arg	Thr	Ala	His	Tyr	Asp	Tyr	Trp	Ser		
				165					170					175			
gat	acc	gtg	cgc	cgt	tcc	gtg	ctg	gtg	gat	tcg	aaa	gcc	gac	atg	ctg	576	
Asp	Thr	Val	Arg	Arg	Ser	Val	Leu	Val	Asp	Ser	Lys	Ala	Asp	Met	Leu		
			180					185					190				
atg	ttt	ggt	aac	ggt	gag	cgt	ccg	ctg	gtg	gaa	gtg	gcg	cat	cgt	ctg	624	
Met	Phe	Gly	Asn	Gly	Glu	Arg	Pro	Leu	Val	Glu	Val	Ala	His	Arg	Leu		
		195					200					205					
gcg	atg	ggc	gag	cca	att	agt	gaa	atc	cgc	gat	gtg	cgt	aat	acc	gcg	672	
Ala	Met	Gly	Glu	Pro	Ile	Ser	Glu	Ile	Arg	Asp	Val	Arg	Asn	Thr	Ala		
		210				215					220						
att	atc	gtg	aaa	gag	gcg	ctg	cct	ggc	tgg	agc	ggc	gtg	gat	tcc	acc	720	
Ile	Ile	Val	Lys	Glu	Ala	Leu	Pro	Gly	Trp	Ser	Gly	Val	Asp	Ser	Thr		
		225			230					235					240		
cgt	ctt	gat	acc	cct	gga	aaa	atc	gac	cca	atc	ccg	cat	ccg	tat	ggt	768	
Arg	Leu	Asp	Thr	Pro	Gly	Lys	Ile	Asp	Pro	Ile	Pro	His	Pro	Tyr	Gly		
				245					250					255			
gaa	gat	ttg	ccg	tgc	gcg	gat	aac	aaa	ccg	gtg	gca	ccg	aaa	aag	cag	816	
Glu	Asp	Leu	Pro	Cys	Ala	Asp	Asn	Lys	Pro	Val	Ala	Pro	Lys	Lys	Gln		
			260					265					270				
gaa	gcc	aaa	gcc	gta	acc	gtg	cag	cca	ccg	cgc	ccg	aaa	ccg	tgg	gaa	864	
Glu	Ala	Lys	Ala	Val	Thr	Val	Gln	Pro	Pro	Arg	Pro	Lys	Pro	Trp	Glu		
		275					280					285					
aaa	acc	tac	gtg	ttg	ctg	cct	tct	ttc	gag	aaa	gtg	aag	ggc	gat	aaa	912	
Lys	Thr	Tyr	Val	Leu	Leu	Pro	Ser	Phe	Glu	Lys	Val	Lys	Gly	Asp	Lys		
		290				295					300						
gtg	ctg	tac	gcc	cat	gct	tcg	cgt	att	ctg	cac	cac	gaa	acc	aac	cca	960	
Val	Leu	Tyr	Ala	His	Ala	Ser	Arg	Ile	Leu	His	His	Glu	Thr	Asn	Pro		
		305			310					315					320		
gct	gtg	ccc	gcg	cat	tga											978	
Ala	Val	Pro	Ala	His	*												
				325													

<210> 153

<211> 681
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(681)

<400> 153

atg att cag tat ctg aac gtc ttt ttt tac gat atc tac ccg tac att	48
Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile	
1 5 10 15	
tgt gcg acg gtg ttt ttc ctc ggc agc tgg ctg cgc tac gac tac ggg	96
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly	
20 25 30	
cag tac acc tgg cgc gcc tcc tca agt caa atg ctc gat aaa cgc ggg	144
Gln Tyr Thr Trp Arg Ala Ser Ser Ser Gln Met Leu Asp Lys Arg Gly	
35 40 45	
atg gtg ata tgg tcg aat ctg ttc cat atc ggc att ttg ggg att ttc	192
Met Val Ile Trp Ser Asn Leu Phe His Ile Gly Ile Leu Gly Ile Phe	
50 55 60	
ttc ggg cac ttg ttc ggc atg tta acg ccg cac tgg atg tac gcg tgg	240
Phe Gly His Leu Phe Gly Met Leu Thr Pro His Trp Met Tyr Ala Trp	
65 70 75 80	
ttt ttg cca gtg gca gcg aaa caa ctc atg gcg atg gtg ctc ggc ggt	288
Phe Leu Pro Val Ala Ala Lys Gln Leu Met Ala Met Val Leu Gly Gly	
85 90 95	
att tgc ggt gtg ttg acg ttg att ggc ggc gca gga ctg ctg tgg cgc	336
Ile Cys Gly Val Leu Thr Leu Ile Gly Gly Ala Gly Leu Leu Trp Arg	
100 105 110	
agg ctg aca aat cag cgc gtg cgt gcc act tcc act acg ccg gat atc	384
Arg Leu Thr Asn Gln Arg Val Arg Ala Thr Ser Thr Thr Pro Asp Ile	
115 120 125	
atc atc atg agc att ttg ctg atc cag tgt ctg ttg ggg cta agt acc	432
Ile Ile Met Ser Ile Leu Leu Ile Gln Cys Leu Leu Gly Leu Ser Thr	
130 135 140	
ata ccg ttt tca gca cag tat cct gat ggt agc gaa atg atg aag ctg	480
Ile Pro Phe Ser Ala Gln Tyr Pro Asp Gly Ser Glu Met Met Lys Leu	
145 150 155 160	
gtg ggt tgg gcg caa agc att gtc act ttc cgt ggt gga tcg tca gag	528
Val Gly Trp Ala Gln Ser Ile Val Thr Phe Arg Gly Gly Ser Ser Glu	
165 170 175	
atg ctc aac ggc gta gcg ttc gtc ttc cgc ctg cat ctg gtg ttg gga	576
Met Leu Asn Gly Val Ala Phe Val Phe Arg Leu His Leu Val Leu Gly	
180 185 190	

atg acc atc ttc ctg ctc ttc ccg ttc acc cga ctg gtg cat gtg tgg	624
Met Thr Ile Phe Leu Leu Phe Pro Phe Thr Arg Leu Val His Val Trp	
195 200 205	

agc gcg ccg ttt gag tac ttt act cgt cga tat caa att gtg cgt tcg	672
Ser Ala Pro Phe Glu Tyr Phe Thr Arg Arg Tyr Gln Ile Val Arg Ser	
210 215 220	

cgg cga taa	681
Arg Arg *	
225	

<210> 154
 <211> 696
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(696)

<400> 154	
atg cag atc ctc aaa gtg atc ggc ctg ttg atg gag tat ccg gac gag	48
Met Gln Ile Leu Lys Val Ile Gly Leu Leu Met Glu Tyr Pro Asp Glu	
1 5 10 15	

ctg ttg tgg gaa tgc aag gag gac gcg ctg gcg ttg atc cgc cgc gac	96
Leu Leu Trp Glu Cys Lys Glu Asp Ala Leu Ala Leu Ile Arg Arg Asp	
20 25 30	

gcg ccg atg ctt acg gat ttc acc cac aac ctg ctt aac gcg ccg ctg	144
Ala Pro Met Leu Thr Asp Phe Thr His Asn Leu Leu Asn Ala Pro Leu	
35 40 45	

ctg gat aaa cag gcc gaa tgg tgc gaa gtg ttt gac cgc ggg cgc acc	192
Leu Asp Lys Gln Ala Glu Trp Cys Glu Val Phe Asp Arg Gly Arg Thr	
50 55 60	

acg tcg ctg ctg ctg ttc gaa cat gtt cat gcc gag tcc cgc gat cgc	240
Thr Ser Leu Leu Leu Phe Glu His Val His Ala Glu Ser Arg Asp Arg	
65 70 75 80	

ggc cag gca atg gtg gac ctg ctg gcg gag tat gaa aag gtc ggc ctg	288
Gly Gln Ala Met Val Asp Leu Leu Ala Glu Tyr Glu Lys Val Gly Leu	
85 90 95	

cag ctg gat tgt cgg gaa ctg ccc gat tat cta ccg ctg tat ctg gag	336
Gln Leu Asp Cys Arg Glu Leu Pro Asp Tyr Leu Pro Leu Tyr Leu Glu	
100 105 110	

tat tta agc gta ctg cct gac gat cag gcg aaa gaa gga ttg ctc aat	384
Tyr Leu Ser Val Leu Pro Asp Asp Gln Ala Lys Glu Gly Leu Leu Asn	
115 120 125	

gtt gcg ccg atc ctc gcc ctg ctt ggc ggt cgc tta aaa caa cgc gag	432
Val Ala Pro Ile Leu Ala Leu Leu Gly Gly Arg Leu Lys Gln Arg Glu	

130	135	140	
gca ccg tgg tac gcg ttg ttt gat gct ctg ctg caa ctg gcg gga agc			480
Ala Pro Trp Tyr Ala Leu Phe Asp Ala Leu Leu Gln Leu Ala Gly Ser			
145	150	155	160
tcc ctt tca agt gac agt gtc aca aaa caa gta aac agc gaa gag cgc			528
Ser Leu Ser Ser Asp Ser Val Thr Lys Gln Val Asn Ser Glu Glu Arg			
	165	170	175
gat gac acc cgc cag gcg ctt gat gca gtg tgg gaa gag gaa cag gtg			576
Asp Asp Thr Arg Gln Ala Leu Asp Ala Val Trp Glu Glu Glu Gln Val			
	180	185	190
aag ttt att gaa gat aac gcc acg gcg tgt gac agc tcg ccg ctt aat			624
Lys Phe Ile Glu Asp Asn Ala Thr Ala Cys Asp Ser Ser Pro Leu Asn			
	195	200	205
caa tat cag cga cgc ttt agc cag gat gtc gcg ccg caa tat gtc gac			672
Gln Tyr Gln Arg Arg Phe Ser Gln Asp Val Ala Pro Gln Tyr Val Asp			
	210	215	220
atc agt gcg gga ggt ggg aaa tga			696
Ile Ser Ala Gly Gly Gly Lys *			
225	230		
<210> 155			
<211> 1545			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(1545)			
<400> 155			
atg aaa atc cgt tca caa gtc ggc atg gtg ctt aac ctc gac aaa tgt			48
Met Lys Ile Arg Ser Gln Val Gly Met Val Leu Asn Leu Asp Lys Cys			
1	5	10	15
atc ggc tgc cat acc tgt tcg gtg acc tgt aaa aac gtc tgg acc ggg			96
Ile Gly Cys His Thr Cys Ser Val Thr Cys Lys Asn Val Trp Thr Gly			
	20	25	30
cgc gaa ggc atg gag tac gca tgg ttt aac aac gtc gaa acc aaa ccg			144
Arg Glu Gly Met Glu Tyr Ala Trp Phe Asn Asn Val Glu Thr Lys Pro			
	35	40	45
ggc att ggt tat ccg aaa aac tgg gaa gat cag gaa gag tgg caa ggc			192
Gly Ile Gly Tyr Pro Lys Asn Trp Glu Asp Gln Glu Glu Trp Gln Gly			
	50	55	60
ggc tgg gtg cgt gat gtg aat ggc aag ata cgc ccg cgt ctg ggc aac			240
Gly Trp Val Arg Asp Val Asn Gly Lys Ile Arg Pro Arg Leu Gly Asn			
65	70	75	80

<211> 3741
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3741)

<400> 156
 atg agt aaa ctt ttg gat cgc ttt cgc tac ttc aaa caa aag ggc gaa 48
 Met Ser Lys Leu Leu Asp Arg Phe Arg Tyr Phe Lys Gln Lys Gly Glu
 1 5 10 15

acc ttt gcc gat ggt cac gga cag gtg atg cat agc aac cgc gac tgg 96
 Thr Phe Ala Asp Gly His Gly Gln Val Met His Ser Asn Arg Asp Trp
 20 25 30

gag gac agc tat cgc cag cgt tgg cag ttc gac aaa atc gtg cgt tcc 144
 Glu Asp Ser Tyr Arg Gln Arg Trp Gln Phe Asp Lys Ile Val Arg Ser
 35 40 45

acc cac ggt gtt aac tgt aca ggc tcc tgt agc tgg aaa atc tac gtt 192
 Thr His Gly Val Asn Cys Thr Gly Ser Cys Ser Trp Lys Ile Tyr Val
 50 55 60

aaa aat ggt ctg gtg acc tgg gaa atc caa cag acc gac tac ccg cgc 240
 Lys Asn Gly Leu Val Thr Trp Glu Ile Gln Gln Thr Asp Tyr Pro Arg
 65 70 75 80

act cgc cct gac ctg ccc aat cat gaa cct cgc ggc tgc ccg cgt ggc 288
 Thr Arg Pro Asp Leu Pro Asn His Glu Pro Arg Gly Cys Pro Arg Gly
 85 90 95

gca agt tac tcc tgg tat ctt tac agc gct aac cgc ctg aaa tac ccg 336
 Ala Ser Tyr Ser Trp Tyr Leu Tyr Ser Ala Asn Arg Leu Lys Tyr Pro
 100 105 110

ctc att cgt aaa cga ctg att gaa ctg tgg cgc gaa gcc ctc aag caa 384
 Leu Ile Arg Lys Arg Leu Ile Glu Leu Trp Arg Glu Ala Leu Lys Gln
 115 120 125

cac agc gat ccg gta ctg gcg tgg gca tcg att atg aac gat ccg caa 432
 His Ser Asp Pro Val Leu Ala Trp Ala Ser Ile Met Asn Asp Pro Gln
 130 135 140

aag tgc ctg agc tac aaa caa gtg cgt ggg cgc ggc ggc ttt atc cgc 480
 Lys Cys Leu Ser Tyr Lys Gln Val Arg Gly Arg Gly Gly Phe Ile Arg
 145 150 155 160

tcc aac tgg cag gaa cta aac cag ctg att gcc gcc gct aac gtc tgg 528
 Ser Asn Trp Gln Glu Leu Asn Gln Leu Ile Ala Ala Ala Asn Val Trp
 165 170 175

acc atc aaa acc tac ggc ccg gat cgc gtt gcc ggt ttc tcg ccg atc 576
 Thr Ile Lys Thr Tyr Gly Pro Asp Arg Val Ala Gly Phe Ser Pro Ile
 180 185 190

CCDS: E37410

ccg gcg atg tgc atg gtt tct tac gcc gcc gga acg cgt tat ctg tgc	624
Pro Ala Met Ser Met Val Ser Tyr Ala Ala Gly Thr Arg Tyr Leu Ser	
195 200 205	
ctg ctt ggc ggc acc tgt tta agt ttc tac gac tgg tat tgc gac ctg	672
Leu Leu Gly Gly Thr Cys Leu Ser Phe Tyr Asp Trp Tyr Cys Asp Leu	
210 215 220	
ccg ccc gcc tgc ccg atg acc tgg ggc gag caa acc gac gta ccg gaa	720
Pro Pro Ala Ser Pro Met Thr Trp Gly Glu Gln Thr Asp Val Pro Glu	
225 230 235 240	
tct gcc gac tgg tat aac tcc agc tac atc atc gcc tgg ggg tct aac	768
Ser Ala Asp Trp Tyr Asn Ser Ser Tyr Ile Ile Ala Trp Gly Ser Asn	
245 250 255	
gta ccg cag aca cgt acg ccg gac gcc cac ttc ttt acc gaa gta cgc	816
Val Pro Gln Thr Arg Thr Pro Asp Ala His Phe Phe Thr Glu Val Arg	
260 265 270	
tac aaa ggc act aaa acc atc gcc att acc cct gac tac tct gaa gtg	864
Tyr Lys Gly Thr Lys Thr Ile Ala Ile Thr Pro Asp Tyr Ser Glu Val	
275 280 285	
gcc aaa ttg tgc gac cag tgg ctg gca ccg aaa caa ggc act gat agc	912
Ala Lys Leu Cys Asp Gln Trp Leu Ala Pro Lys Gln Gly Thr Asp Ser	
290 295 300	
gcc ctg gcg atg gca atg ggc cat gtg att tta aaa gag ttt cat ctc	960
Ala Leu Ala Met Ala Met Gly His Val Ile Leu Lys Glu Phe His Leu	
305 310 315 320	
gat aat ccc agc gac tac ttt atc aac tac tgc cgc cgc tac agc gac	1008
Asp Asn Pro Ser Asp Tyr Phe Ile Asn Tyr Cys Arg Arg Tyr Ser Asp	
325 330 335	
atg ccg atg ctg gta atg ctg gag cct cgc gac gat ggt agc tac gtt	1056
Met Pro Met Leu Val Met Leu Glu Pro Arg Asp Asp Gly Ser Tyr Val	
340 345 350	
ccc ggg cgc atg atc cgc gca tct gac ctg gtg gat gga ctg ggc gaa	1104
Pro Gly Arg Met Ile Arg Ala Ser Asp Leu Val Asp Gly Leu Gly Glu	
355 360 365	
agc aac aat ccg cag tgg aaa acc gta gca gtt aat acc gca ggt gaa	1152
Ser Asn Asn Pro Gln Trp Lys Thr Val Ala Val Asn Thr Ala Gly Glu	
370 375 380	
ttg gta gtg ccg aac ggt tgc att ggt ttc cgc tgg gga gaa aaa ggc	1200
Leu Val Val Pro Asn Gly Ser Ile Gly Phe Arg Trp Gly Glu Lys Gly	
385 390 395 400	
aaa tgg aat ctg gaa tcc att gcc gcc ggt acg gaa acc gaa ttg tgc	1248
Lys Trp Asn Leu Glu Ser Ile Ala Ala Gly Thr Glu Thr Glu Leu Ser	
405 410 415	
tta acc ctg ctc ggt caa cat gac gct gtt gca ggc gtg gcc ttc ccc	1296

ctg gaa cat ggc tta ccg ccg aca gca ggt ctg gga att ggt atc gac	1440
Leu Glu His Gly Leu Pro Pro Thr Ala Gly Leu Gly Ile Gly Ile Asp	
465 470 475 480	

cgt atg gta atg ctg ttc acc aac agc cat acc atc cgc gac gtt att	1488
Arg Met Val Met Leu Phe Thr Asn Ser His Thr Ile Arg Asp Val Ile	
485 490 495	

ctg ttc ccg gcg atg cgt ccg gta aaa taa	1518
Leu Phe Pro Ala Met Arg Pro Val Lys *	
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Met Phe Glu Ile Asn Pro Val Asn Asn Arg Ile Gln Asp Leu Thr Glu	
1 5 10 15	

cgc tcc gac gtt ctt agg ggg tat ctt gac tac gac gcc aag aaa gag	96
Arg Ser Asp Val Leu Arg Gly Tyr Leu Asp Tyr Asp Ala Lys Lys Glu	
20 25 30	

cgt ctg gaa gaa gta aac gcc gag ctg gaa cag ccg gat gtc tgg aac	144
Arg Leu Glu Glu Val Asn Ala Glu Leu Glu Gln Pro Asp Val Trp Asn	
35 40 45	

gaa ccc gaa cgc gca cag gcg ctg ggt aaa gag cgt tcc tcc ctc gaa	192
Glu Pro Glu Arg Ala Gln Ala Leu Gly Lys Glu Arg Ser Ser Leu Glu	
50 55 60	

gcc gtt gtc gac acc ctc gac caa atg aaa cag ggg ctg gaa gat gtt	240
Ala Val Val Asp Thr Leu Asp Gln Met Lys Gln Gly Leu Glu Asp Val	
65 70 75 80	

tct ggt ctg ctg gaa ctg gct gta gaa gct gac gac gaa gaa acc ttt	288
Ser Gly Leu Leu Glu Leu Ala Val Glu Ala Asp Asp Glu Glu Thr Phe	
85 90 95	

aac gaa gcc gtt gct gaa ctc gac gcc ctg gaa gaa aaa ctg gcg cag	336
Asn Glu Ala Val Ala Glu Leu Asp Ala Leu Glu Glu Lys Leu Ala Gln	
100 105 110	

ctt gag ttc cgc cgt atg ttc tct ggc gaa tat gac agc gcc gac tgc	384
Leu Glu Phe Arg Arg Met Phe Ser Gly Glu Tyr Asp Ser Ala Asp Cys	
115 120 125	

tac ctc gat att cag gcg ggg tct ggc ggt acg gaa gca cag gac tgg	432
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355

360

365

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 <211> 1734
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 1 5 10 15

gac ttg ccc gct gaa ttg cct ccc ttg ctg cgc cgt tta tac gcc agc 96
 Asp Leu Pro Ala Glu Leu Pro Pro Leu Leu Arg Arg Leu Tyr Ala Ser
 20 25 30

cgg gga gta cgc agt gcg caa gaa ctg gaa cgc agt gtt aaa ggt atg 144
 Arg Gly Val Arg Ser Ala Gln Glu Leu Glu Arg Ser Val Lys Gly Met
 35 40 45

ctg ccc tgg cag caa ctg agc ggc gtc gaa aag gcc gtt gag atc ctt 192
 Leu Pro Trp Gln Gln Leu Ser Gly Val Glu Lys Ala Val Glu Ile Leu
 50 55 60

tac aac gct ttt cgc gaa gga acg cgg att att gtg gtc ggt gat ttc 240
 Tyr Asn Ala Phe Arg Glu Gly Thr Arg Ile Ile Val Val Gly Asp Phe
 65 70 75 80

gac gcc gac ggc gcg acc agc acg gct cta agc gtg ctg gcg atg cgc 288
 Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg
 85 90 95

tcg ctt ggt tgc agc aat atc gac tac ctg gta cca aac cgt ttc gaa 336
 Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu
 100 105 110

gac ggt tac ggc tta agc ccg gaa gtg gtc gat cag gcc cat gcc cgt 384
 Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg
 115 120 125

ggc gcg cag tta att gtc acg gtg gat aac ggt att tcc tcc cat gcg 432
 Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala
 130 135 140

ggg gtt gag cac gct cgc tcg ttg ggc atc ccg gtt att gtt acc gat 480
 Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp
 145 150 155 160

cac cat ttg cca ggc gac aca tta ccc gca gcg gaa gcg atc att aac 528
 His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn
 165 170 175

cct aac ttg cgc gac tgt aat ttc ccg tcg aaa tca ctg gca ggc gtg	576
Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val	
180 185 190	
ggt gtg gcg ttt tat ctg atg ctg gcg ctg cgc acc ttt ttg cgc gat	624
Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp	
195 200 205	
cag ggc tgg ttt gat gag cgt aac atc gca att cct aac ctg gca gaa	672
Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu	
210 215 220	
ctg ctg gat ctg gtc gcg ctg ggg aca gtg gcg gac gtc gtg ccg ctg	720
Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu	
225 230 235 240	
gac gct aat aat cgc att ctg acc tgg cag ggg atg agt cgc atc cga	768
Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg	
245 250 255	
gcc gga aag tgc cgt ccg ggg att aaa gcg ctg ctt gaa gtg gca aac	816
Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn	
260 265 270	
cgt gat gca caa aaa ctc gcc gcc agc gat tta ggt ttt gcg ctg ggg	864
Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly	
275 280 285	
cca cgt ctc aat gct gcc gga cga ctg gac gat atg tcc gtc ggt gtg	912
Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val	
290 295 300	
gcg ctg ttg ttg tgc gac aac atc ggc gaa gcg cgc gtg ctg gca aat	960
Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn	
305 310 315 320	
gaa ctc gat gcg cta aac cag acg cga aaa gag atc gaa caa gga atg	1008
Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met	
325 330 335	
caa att gaa gcc ctg acc ctg tgc gag aaa ctg gag cgc agc cgt gac	1056
Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp	
340 345 350	
acg cta ccc ggc ggg ctg gca atg tat cac ccc gaa tgg cat cag ggc	1104
Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly	
355 360 365	
gtt gtc ggt att ctg gct tcg cgc atc aaa gag cgt ttt cac cgt ccg	1152
Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro	
370 375 380	
gtt atc gcg ttt gcg cca gca ggt gac ggt acg ctg aaa ggt tcc ggt	1200
Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly	
385 390 395 400	

[illegible]

119

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Thr	Gly	Asp	Phe	Gln	Lys	Glu	Leu	Ala	Tyr	Leu	Gln	Asn	Val	Ile	Leu	
65					70					75					80	
tat	aat	gtc	tcg	tct	ctt	cgt	ctg	gat	ttt	tta	ggt	tat	aac	gcc	caa	288
Tyr	Asn	Val	Ser	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Gly	Tyr	Asn	Ala	Gln	
				85					90					95		
att	att	caa	cga	tcg	gac	aat	act	tgt	gaa	ctt	acc	att	aat	gaa	ccg	336
Ile	Ile	Gln	Arg	Ser	Asp	Asn	Thr	Cys	Glu	Leu	Thr	Ile	Asn	Glu	Pro	
			100					105					110			
tta	aaa	aac	cag	gaa	ata	tcc	aca	ggt	aat	atc	aat	att	aat	tgc	cca	384
Leu	Lys	Asn	Gln	Glu	Ile	Ser	Thr	Gly	Asn	Ile	Asn	Ile	Asn	Cys	Pro	
		115					120					125				
tta	aaa	gat	att	tac	aat	gaa	atc	agg	agg	tta	aac	gta	att	ttt	agt	432
Leu	Lys	Asp	Ile	Tyr	Asn	Glu	Ile	Arg	Arg	Leu	Asn	Val	Ile	Phe	Ser	
		130				135					140					
tgt	ggg	act	gga	gat	atc	gtt	gat	cta	tcc	tct	ctg	gac	tta	cgt	aat	480
Cys	Gly	Thr	Gly	Asp	Ile	Val	Asp	Leu	Ser	Ser	Leu	Asp	Leu	Arg	Asn	
145					150					155					160	
gtc	gat	tta	gat	tat	tat	gat	ttc	aca	gat	aaa	cat	atg	gct	aat	act	528
Val	Asp	Leu	Asp	Tyr	Tyr	Asp	Phe	Thr	Asp	Lys	His	Met	Ala	Asn	Thr	
				165					170					175		
att	tta	aat	cct	ttt	aaa	ttg	aat	tca	aca	aat	ttt	act	aat	gcc	aac	576
Ile	Leu	Asn	Pro	Phe	Lys	Leu	Asn	Ser	Thr	Asn	Phe	Thr	Asn	Ala	Asn	
			180					185					190			
atg	ttt	cag	gtt	aat	ttt	gtt	agt	tca	aca	caa	aac	gcc	aca	atc	tcc	624
Met	Phe	Gln	Val	Asn	Phe	Val	Ser	Ser	Thr	Gln	Asn	Ala	Thr	Ile	Ser	
		195					200					205				
tgg	gat	tat	tta	cta	aaa	ata	acg	cct	gtt	tta	ata	agc	att	agc	gat	672
Trp	Asp	Tyr	Leu	Leu	Lys	Ile	Thr	Pro	Val	Leu	Ile	Ser	Ile	Ser	Asp	
	210					215					220					
atg	tat	tct	gaa	gaa	aaa	atc	aag	ttt	gtc	gaa	agt	tgt	tta	aat	gag	720
Met	Tyr	Ser	Glu	Glu	Lys	Ile	Lys	Phe	Val	Glu	Ser	Cys	Leu	Asn	Glu	
225					230					235					240	
cct	gga	gac	att	acc	gaa	gaa	caa	tta	aaa	att	atg	aga	ttt	gca	att	768
Pro	Gly	Asp	Ile	Thr	Glu	Glu	Gln	Leu	Lys	Ile	Met	Arg	Phe	Ala	Ile	
				245					250					255		
ata	aaa	tct	ata	cca	agg	gca	act	ctt	aca	gat	aaa	tta	gaa	aat	gaa	816
Ile	Lys	Ser	Ile	Pro	Arg	Ala	Thr	Leu	Thr	Asp	Lys	Leu	Glu	Asn	Glu	
			260					265					270			
tta	aca	aaa	gaa	ata	tat	aaa	agc									

aac aga att aaa tta aca gag atg aaa gaa ttc tca tca gaa aaa ata	912
Asn Arg Ile Lys Leu Thr Glu Met Lys Glu Phe Ser Ser Glu Lys Ile	
290 295 300	
tat gat tac atc gat ata atc att gaa gat tat gaa aat acc aaa gaa	960
Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu	
305 310 315 320	
aat gct tat ctg gtc gtc ccc caa att aat tat act atg gat tta aac	1008
Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn	
325 330 335	
ata gaa gac tct agc tca gaa gag tta ctt tca gat aat acc ctc gag	1056
Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu	
340 345 350	
aaa gac gaa aat tct ccg gac aat ggc ttt gag gtc ggg gaa tat aac	1104
Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn	
355 360 365	
aca tat gaa gca tat aac tca gag aag caa tat ttt acc aga gag gac	1152
Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp	
370 375 380	
tat acg tat gat tac gac ctt tta aat gca ata tag	1188
Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile *	
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Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe	
1 5 10 15	
atg ttt tct ggg ctg tta atc att ctg gtt ccc ctg att gtg ggt tac	96
Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr	
20 25 30	
ctc att ccg ctt cgc caa caa gct gcg tta aaa gtt att aat cag cta	144
Leu Ile Pro Leu Arg Gln Gln Ala Ala Leu Lys Val Ile Asn Gln Leu	
35 40 45	
tta agc tgg atg gtt tac ctt att ctc ttt ttt atg ggt atc agt ctg	192
Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu	
50 55 60	
gcg ttt ctc gat aac ctc gcc agt aac ctg ttg gcg att ctg cat tat	240

225	230							235							240			
acc atg act tta atg gcg ctg ggc atg ttg cca aaa gcg cat ccg ttg	Thr Met Thr Leu Met Ala Leu Gly Met Leu Pro Lys Ala His Pro Leu	768																
245				250				255										
tcg ctg ggt atg ctg ggg atg cac ggc gtg cgc agc acc aac tat att	Ser Leu Gly Met Leu Gly Met His Gly Val Arg Ser Thr Asn Tyr Ile	816																
260				265				270										
ttg cag gag gcg gat ttg ttg ata gtg ctc ggt gcg cgt ttt gat gac	Leu Gln Glu Ala Asp Leu Leu Ile Val Leu Gly Ala Arg Phe Asp Asp	864																
275				280				285										
cgg gcg att ggc aaa acc gag cag ttc tgt ccg aat gcc aaa atc att	Arg Ala Ile Gly Lys Thr Glu Gln Phe Cys Pro Asn Ala Lys Ile Ile	912																
290				295				300										
cat gtc gat atc gac cgt gca gag ctg ggt aaa atc aag cag ccg cac	His Val Asp Ile Asp Arg Ala Glu Leu Gly Lys Ile Lys Gln Pro His	960																
305				310				315				320						
gtg gcg att cag gcg gat gtt gat gac gtg ctg gcg cag ttg atc ccg	Val Ala Ile Gln Ala Asp Val Asp Asp Val Leu Ala Gln Leu Ile Pro	1008																
325				330				335										
ctg gtg gaa gcg caa ccg cgt gca gag tgg cac cag ttg gta gcg gat	Leu Val Glu Ala Gln Pro Arg Ala Glu Trp His Gln Leu Val Ala Asp	1056																
340				345				350										
ttg cag cgt gag ttt ccg tgt cca atc ccg aaa gcg tgc gat ccg tta	Leu Gln Arg Glu Phe Pro Cys Pro Ile Pro Lys Ala Cys Asp Pro Leu	1104																
355				360				365										
agc cat tac ggc ctg atc aac gcc gtt gcc gcc tgt gtc gat gac aat	Ser His Tyr Gly Leu Ile Asn Ala Val Ala Ala Cys Val Asp Asp Asn	1152																
370				375				380										
gca att atc acc acc gac gtt ggt cag cat cag atg tgg acc gcg caa	Ala Ile Ile Thr Thr Asp Val Gly Gln His Gln Met Trp Thr Ala Gln	1200																
385				390				395				400						
gct tat ccg ctc aat cgc cca cgc cag tgg ctg acc tcc ggt ggg ctg	Ala Tyr Pro Leu Asn Arg Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu	1248																
405				410				415										
ggc acg atg ggt ttt ggc ctg cct gcg gcg att ggc gct gcg ctg gcg	Gly Thr Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ala Leu Ala	1296																
420				425				430										
aac ccg gat cgc aaa gtg ttg tgt ttc tcc ggc gac ggc agc ctg atg	Asn Pro Asp Arg Lys Val Leu Cys Phe Ser Gly Asp Gly Ser Leu Met	1344																
435				440				445										
atg aat att cag gag atg gcg acc gcc agt gaa aat cag ctg gat gtc	Met Asn Ile Gln Glu Met Ala Thr Ala Ser Glu Asn Gln Leu Asp Val	1392																
450				455				460										

<220>
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 <222> (1)...(1017)

<400> 172

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Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln	
1 5 10 15	
ctt acc ttc gcc gac agt gaa ttc agc agt aag cgc cgt cag acc aga	96
Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg	
20 25 30	
aaa gag att ttc ttg tcc cgc atg gag cag att ctg cca tgg caa aac	144
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn	
35 40 45	
atg gtg gaa gtc atc gag ccg ttt tac ccc aag gct ggt aat ggc cgg	192
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg	
50 55 60	
cga cct tat ccg ctg gaa acc atg cta cgc att cac tgc atg cag cat	240
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His	
65 70 75 80	
tgg tac aac ctg agc gat ggc gcg atg gaa gat gct ctg tac gaa atc	288
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile	
85 90 95	
gcc tcc atg cgt ctg ttt gcc cgg tta tcc ctg gat agc gcc ttg ccg	336
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro	
100 105 110	
gac cgc acc acc atc atg aat ttc cgc cac ctg ctg gag cag cat caa	384
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln	
115 120 125	
ctg gcc cgc caa ttg ttc aag acc atc aat cgc tgg ctg gcc gaa gca	432
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala	
130 135 140	
ggc gtc atg atg act caa ggc acc ttg gtc gat gcc acc atc att gag	480
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu	
145 150 155 160	
gca ccc agc tcg acc aag aac aaa gag cag caa cgc gat ccg gag atg	528
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met	
165 170 175	
cat cag acc aag aaa ggc aat cag tgg cac ttt ggc atg aag gcc cac	576
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His	
180 185 190	
att ggt gtc gat gcc aag agt ggc ctg acc cac agc ctg gtc acc acc	624
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr	
195 200 205	

gcg gcc aac gag cat gac ctc aat cag ctg ggt aat ctg ctg cat gga	672
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly	
210 215 220	
gag gag caa ttt gtc tca gcc gat gcc ggc tac caa ggg gcg cca cag	720
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln	
225 230 235 240	
cgc gag gag ctg gcc gag gtg gat gtg gac tgg ctg atc gcc gag cgc	768
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg	
245 250 255	
ccc ggc aag gta aga acc ttg aaa cag cat cca cgc aag aac aaa acg	816
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr	
260 265 270	
gcc atc aac atc gaa tac atg aaa gcc agc atc cgg gcc agg gtg gag	864
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu	
275 280 285	
cac cca ttt cgc atc atc aag cga cag ttc ggc ttc gtg aaa gcc aga	912
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg	
290 295 300	
tac aag ggg ttg ctg aaa aac gat aac caa ctg gcg atg tta ttc acg	960
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr	
305 310 315 320	
ctg gcc aac ctg ttt cgg gcg gac caa atg ata cgt cag tgg gag aga	1008
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg	
325 330 335	
tct cac taa	1017
Ser His *	

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 <211> 474
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(474)

<400> 173	
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1 5 10 15	
aaa tta ctc gaa aat ctt aat gct gac gat gag cac tac aag att atc	96
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile	
20 25 30	
gta cgc gac aac aaa gac tct cta tta ttg aaa caa ata tgc cag cat	144

gac	tcc	atg	aca	ata	gaa	act	tat	aag	caa	att	agt	gag	aat	aca	aaa	912
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys	
	290					295					300					

att	att	tct	cag	aaa	att	cga	aca	gga	agt	tac	ttc	agg	gat	gtt	ctt	960
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu	
	305				310					315					320	

gaa	gag	gtg	atc	gat	gat	ctt	aaa	act	cgc	taa						993
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg	*						
				325					330							

<210> 177
 <211> 1167
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)...(1167)

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Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys	
	1			5					10					15		

tta	tat	ctt	aag	aag	gat	ata	ttt	tat	cca	gcc	gta	tgc	gtt	aat	atc	96
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile	
			20					25					30			

atc	ttc	gca	ctg	gtc	tta	ttg	gga	tat	gaa	ata	acg	tca	gat	ata	tat	144
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr	
		35					40					45				

gct	ttt	cag	tta	aat	gac	gct	acg	ttg	att	ttt	cta	ctt	tgc	aat	gtt	192
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val	
	50				55						60					

ttg	aca	ttt	acc	ctg	tca	tgt	tta	ttg	acg	gaa	agt	gta	tta	gat	cta	240
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu	
	65				70				75					80		

aat	atc	aga	aaa	gtc	aat	aat	gct	att	tat	agc	ata	cca	tcg	aag	aaa	288
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys	
				85				90						95		

gtg	cat	aat	gta	ggc	ttg	tta	gtt	att	tct	ttt	tcg	atg	ata	tat	ata	336
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile	
			100					105					110			

tgc	atg	agg	tta	agt	aac	tac	cag	ttc	ggg	act	agc	tta	ctt	agc	tat	384
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr	
		115					120					125				

atg	aat	ttg	ata	aga	gat	gct	gat	gtt	gaa	gac	aca	tca	aga	aat	ttc	432
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe	

130	135	140	
tca gca tac atg cag cca atc att cta act act ttt gct tta ttt att			480
Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile			
145	150	155	160
tgg tct aaa aaa ttt act aat aca aag gta agt aaa aca ttt act tta			528
Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu			
	165	170	175
ctt gtt ttt att gta ttc atc ttt gca att ata ctg aat act ggt aag			576
Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys			
	180	185	190
caa att gtc ttt atg gtt atc atc tct tat gca ttc atc gta ggt gtt			624
Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val			
	195	200	205
aat aga gta aaa cat tat gtt tat ctt att aca gct gta ggt gtt cta			672
Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu			
	210	215	220
ttc tcc ttg tat atg ctc ttt tta cgt gga ctg cct ggg ggg atg gca			720
Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala			
	225	230	240
tat tat cta tcc atg tat ttg gtc agc cct ata atc gcg ttt cag gag			768
Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu			
	245	250	255
ttt tat ttt cag caa gta tct aac tct gcc agt tct cat gtc ttt tgg			816
Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp			
	260	265	270
ttt ttt gaa agg ctg atg ggg cta tta aca ggt gga gtc tct atg tcg			864
Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser			
	275	280	285
ttg cat aaa gaa ttt gtg tgg gtg ggt ttg cca aca aat gtt tat act			912
Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr			
	290	295	300
gct ttt tcg gat tat gtt tat att tcc gcg gag cta agc tat ttg atg			960
Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met			
	305	310	315
atg gtt att cat ggc tgt att tca ggt gtt tta tgg aga ttg tct cga			1008
Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg			
	325	330	335
aat tac ata tct gtg aaa ata ttt tat tca tat ttt att tat acc ttt			1056
Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe			
	340	345	350
tct ttc att ttt tat cat gaa agc ttc atg act aat att agc agt tgg			1104
Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp			
	355	360	365

ata caa ata act ctt tgt atc ata gta ttc tct caa ttt ctt aag gcc 1152
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380

cag aaa ata aag tga 1167
 Gln Lys Ile Lys *
 385

<210> 178
 <211> 1104
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1104)

<400> 178
 atg tac gat tat atc att gtt ggt tct ggt ttg ttt ggt gcc gtt tgt 48
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15

gcg aat gag tta aaa aag cta aac aaa aaa gtt tta gtg att gag aaa 96
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30

aga aat cat atc ggt gga aat gcg tac aca gag gac tgt gag ggt atc 144
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45

cag att cat aaa tat ggt gca cat att ttt cat acc aat gat aaa tat 192
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60

ata tgg gat tac gtt aat gat tta gta gaa ttt aat cgt ttt act aat 240
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80

tct cca ctg gcg att tat aaa gac aaa tta ttc aac ctt cct ttt aat 288
 Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95

atg aat act ttc cac caa atg tgg gga gtt aaa gat cct caa gaa gct 336
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110

caa aat atc att aat gct cag aaa aaa aag tat ggt gac aag gta cct 384
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125

gaa aat ttg gag gag cag gcg att tca tta gtt ggg gag gac tta tac 432
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140

caa gca ttg ata aag ggt tat acg gag aag cag tgg gga aga agt gca 480

gct gaa gtt ctg gat atg gat atc cgt agc atc tac gcg tac aag caa	624
Ala Glu Val Leu Asp Met Asp Ile Arg Ser Ile Tyr Ala Tyr Lys Gln	
195 200 205	
cga atc gaa aag aga atg ggt ggt aaa ata aac gaa tta ttt att cgt	672
Arg Ile Glu Lys Arg Met Gly Gly Lys Ile Asn Glu Leu Phe Ile Arg	
210 215 220	
tca cat tcg gtc caa cat tga	693
Ser His Ser Val Gln His *	
225 230	

<210> 180
 <211> 1176
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1176)

<400> 180	
atg caa aaa ctc att aac tca gtg caa aac tat gcc tgg ggc agc aaa	48
Met Gln Lys Leu Ile Asn Ser Val Gln Asn Tyr Ala Trp Gly Ser Lys	
1 5 10 15	
acg gcg ttg act gaa ctt tat ggt atg gaa aat ccg tcc agc cag ccg	96
Thr Ala Leu Thr Glu Leu Tyr Gly Met Glu Asn Pro Ser Ser Gln Pro	
20 25 30	
atg gcc gag ctg tgg atg ggc gca cat ccg aaa agc agt tca cga gtg	144
Met Ala Glu Leu Trp Met Gly Ala His Pro Lys Ser Ser Ser Arg Val	
35 40 45	
cag aat gcc gcc gga gat atc gtt tca ctg cgt gat gtg att gag agt	192
Gln Asn Ala Ala Gly Asp Ile Val Ser Leu Arg Asp Val Ile Glu Ser	
50 55 60	
gat aaa tcg act ctg ctc gga gag gcc gtt gcc aaa cgc ttt ggc gaa	240
Asp Lys Ser Thr Leu Leu Gly Glu Ala Val Ala Lys Arg Phe Gly Glu	
65 70 75 80	
ctg cct ttc ctg ttc aaa gta tta tgc gca gca cag cca ctc tcc att	288
Leu Pro Phe Leu Phe Lys Val Leu Cys Ala Ala Gln Pro Leu Ser Ile	
85 90 95	
cag gtt cat cca aac aaa cac aat tct gaa atc ggt ttt gcc aaa gaa	336
Gln Val His Pro Asn Lys His Asn Ser Glu Ile Gly Phe Ala Lys Glu	
100 105 110	
aat gcc gca ggt atc ccg atg gat gcc gcc gag cgt aac tat aaa gat	384
Asn Ala Ala Gly Ile Pro Met Asp Ala Ala Glu Arg Asn Tyr Lys Asp	
115 120 125	
cct aac cac aag ccg gag ctg gtt ttt gcg ctg acg cct ttc ctt gcg	432

cac gtt tcc tga
His Val Ser *
290

876

<210> 183
<211> 726
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(726)

<400> 183
atg gac agt ctc aat ctt aat aaa cat att tcc ggc cag ttc aac gcc 48
Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
1 5 10 15
gaa ctg gaa agt atc cgc acg cag gtg atg acc atg ggc ggc atg gtg 96
Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
20 25 30
gag cag cag ctt tct gat gca atc acc gcg atg cat aac cag gac agc 144
Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
35 40 45
gat ctg gcg aag cgc gtc atc gaa ggc gac aag aac gtc aac atg atg 192
Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
50 55 60
gaa gtg gcg atc gat gaa gcc tgc gtg cgc att atc gcc aaa cgt cag 240
Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
65 70 75 80
ccg acg gcg agc gac ctg cga ctg gtt atg gtg atc agt aaa acc att 288
Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
85 90 95
gcc gag ctg gag cgt att ggc gac gtg gcg gac aaa atc tgc cgt act 336
Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
100 105 110
gcg ctg gag aaa ttc tcc cag cag cat cag ccg ttg ctg gta agt ctg 384
Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
115 120 125
gag tcg ctg ggc cgt cat acc atc cag atg ctg cac gac gtg ctg gac 432
Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
130 135 140
gcg ttc gcg cgg atg gac att gac gaa gcg gta cgt att tat cgt gaa 480
Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
145 150 155 160
gat aaa aaa gtc gat cag gaa tac gaa ggt att gtt cgt caa ctg atg 528

Asp	Lys	Lys	Val	Asp	Gln	Glu	Tyr	Glu	Gly	Ile	Val	Arg	Gln	Leu	Met	
				165					170					175		
acc	tac	atg	atg	gaa	gat	tcg	cgt	acc	att	ccg	agc	gta	ctt	act	gcg	576
Thr	Tyr	Met	Met	Glu	Asp	Ser	Arg	Thr	Ile	Pro	Ser	Val	Leu	Thr	Ala	
			180					185					190			
ctg	ttc	tgc	gcg	cgt	tct	atc	gaa	cgt	att	ggc	gac	cgc	tgc	cag	aat	624
Leu	Phe	Cys	Ala	Arg	Ser	Ile	Glu	Arg	Ile	Gly	Asp	Arg	Cys	Gln	Asn	
		195					200				205					
att	tgt	gag	ttt	atc	ttc	tac	tac	gtg	aag	ggg	cag	gat	ttc	cgt	cac	672
Ile	Cys	Glu	Phe	Ile	Phe	Tyr	Tyr	Val	Lys	Gly	Gln	Asp	Phe	Arg	His	
	210					215					220					
gtc	ggc	ggc	gat	gag	ctg	gat	aaa	ctg	ctg	gcg	ggg	aaa	gat	agc	gac	720
Val	Gly	Gly	Asp	Glu	Leu	Asp	Lys	Leu	Leu	Ala	Gly	Lys	Asp	Ser	Asp	
225					230					235					240	
aaa	taa															726
Lys	*															

<210> 184
 <211> 774
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(774)

<400>	184															
atg	agt	atg	gtt	gaa	act	gcc	ccg	agt	aaa	att	cag	gtt	cgt	aat	ttg	48
Met	Ser	Met	Val	Glu	Thr	Ala	Pro	Ser	Lys	Ile	Gln	Val	Arg	Asn	Leu	
1				5					10					15		
aac	ttc	tac	tac	ggc	aaa	ttc	cat	gcc	ctg	aaa	aac	atc	aac	ctg	gat	96
Asn	Phe	Tyr	Tyr	Gly	Lys	Phe	His	Ala	Leu	Lys	Asn	Ile	Asn	Leu	Asp	
			20					25					30			
atc	gct	aaa	aac	cag	gta	acg	gcg	ttt	atc	ggg	ccg	tcc	ggc	tgc	ggc	144
Ile	Ala	Lys	Asn	Gln	Val	Thr	Ala	Phe	Ile	Gly	Pro	Ser	Gly	Cys	Gly	
		35					40					45				
aaa	tcg	acg	ctg	ctg	cgt	acc	ttc	aac	aaa	atg	ttt	gaa	ctg	tac	ccg	192
Lys	Ser	Thr	Leu	Leu	Arg	Thr	Phe	Asn	Lys	Met	Phe	Glu	Leu	Tyr	Pro	
	50					55				60						
gag	cag	cgt	gcg	gaa	ggc	gaa	att	ctg	ctt	gat	ggc	gac	aac	atc	ctg	240
Glu	Gln	Arg	Ala	Glu	Gly	Glu	Ile	Leu	Leu	Asp	Gly	Asp	Asn	Ile	Leu	
65					70					75					80	
acc	aac	tct	cag	gat	atc	gca	ctg	ctg	cgt	gcg	aaa	gtg	ggc	atg	gtg	288
Thr	Asn	Ser	Gln	Asp	Ile	Ala	Leu	Leu	Arg	Ala	Lys	Val	Gly	Met	Val	
				85					90					95		

ttc cag aaa ccg acg ccg ttt ccg atg tcc atc tac gac aac atc gct	336
Phe Gln Lys Pro Thr Pro Phe Pro Met Ser Ile Tyr Asp Asn Ile Ala	
100 105 110	
ttt ggc gtt cgt ctg ttt gag aag ctc tcc cgt gcc gac atg gac gag	384
Phe Gly Val Arg Leu Phe Glu Lys Leu Ser Arg Ala Asp Met Asp Glu	
115 120 125	
cgc gtg cag tgg gca ttg acc aaa gcc gca ttg tgg aac gaa acc aaa	432
Arg Val Gln Trp Ala Leu Thr Lys Ala Ala Leu Trp Asn Glu Thr Lys	
130 135 140	
gat aaa ttg cac cag agc ggt tac tct ctc tct ggt ggt cag caa cag	480
Asp Lys Leu His Gln Ser Gly Tyr Ser Leu Ser Gly Gly Gln Gln Gln	
145 150 155 160	
cgt ctg tgt att gcg cgt ggt atc gcc att cgc ccg gaa gtg ctg ctg	528
Arg Leu Cys Ile Ala Arg Gly Ile Ala Ile Arg Pro Glu Val Leu Leu	
165 170 175	
ctc gac gaa ccg tgt tcg gcg ctc gac cct atc tct acc ggg cgt att	576
Leu Asp Glu Pro Cys Ser Ala Leu Asp Pro Ile Ser Thr Gly Arg Ile	
180 185 190	
gaa gag ctg atc acc gaa ctg aag cag gat tac acc gtg gtg atc gtc	624
Glu Glu Leu Ile Thr Glu Leu Lys Gln Asp Tyr Thr Val Val Ile Val	
195 200 205	
acc cac aac atg cag cag gct gcg cgt tgt tcc gac cac acg gcg ttt	672
Thr His Asn Met Gln Gln Ala Ala Arg Cys Ser Asp His Thr Ala Phe	
210 215 220	
atg tac ctg ggc gaa ttg att gag ttc agc aac acg gac gat ctg ttc	720
Met Tyr Leu Gly Glu Leu Ile Glu Phe Ser Asn Thr Asp Asp Leu Phe	
225 230 235 240	
acc aag cca gcg aag aaa caa aca gaa gac tac atc acc ggt cgt tac	768
Thr Lys Pro Ala Lys Lys Gln Thr Glu Asp Tyr Ile Thr Gly Arg Tyr	
245 250 255	
ggt tga	774
Gly *	

<210> 185
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> .CDS
 <222> (1)...(891)

<400> 185
 atg gct atg gtt gaa atg caa acc act gcg gcg ctg gct gaa tct cgc 48

Met	Ala	Met	Val	Glu	Met	Gln	Thr	Thr	Ala	Ala	Leu	Ala	Glu	Ser	Arg	
1				5					10					15		
cgc	aaa	atg	cag	gcg	cgt	cgc	cgc	ctc	aaa	aac	cgt	att	gcg	ctg	acg	96
Arg	Lys	Met	Gln	Ala	Arg	Arg	Arg	Leu	Lys	Asn	Arg	Ile	Ala	Leu	Thr	
			20					25					30			
ctc	tcg	atg	gcg	acg	atg	gcc	ttc	ggc	ctg	ttc	tgg	ctg	atc	tgg	att	144
Leu	Ser	Met	Ala	Thr	Met	Ala	Phe	Gly	Leu	Phe	Trp	Leu	Ile	Trp	Ile	
			35				40					45				
tta	atg	tcc	acc	atc	act	cgc	ggc	atc	gac	ggc	atg	tcg	ctg	gcg	ctg	192
Leu	Met	Ser	Thr	Ile	Thr	Arg	Gly	Ile	Asp	Gly	Met	Ser	Leu	Ala	Leu	
	50					55					60					
ttc	act	gaa	atg	acg	ccg	ccg	ccc	aac	acg	gaa	ggc	ggc	ggc	ctg	gcg	240
Phe	Thr	Glu	Met	Thr	Pro	Pro	Pro	Asn	Thr	Glu	Gly	Gly	Gly	Leu	Ala	
	65				70					75					80	
aac	gct	ctg	gcg	ggc	agc	ggc	ctg	tta	att	ttg	tgg	gcc	acg	gta	ttc	288
Asn	Ala	Leu	Ala	Gly	Ser	Gly	Leu	Leu	Ile	Leu	Trp	Ala	Thr	Val	Phe	
				85					90					95		
ggc	acg	ccg	ctg	ggc	att	atg	gcg	ggc	att	tat	ctg	gcg	gaa	tat	ggc	336
Gly	Thr	Pro	Leu	Gly	Ile	Met	Ala	Gly	Ile	Tyr	Leu	Ala	Glu	Tyr	Gly	
			100					105					110			
cgt	aaa	tcc	tgg	ctg	gca	gaa	gtg	att	cgc	ttc	att	aac	gac	att	ctg	384
Arg	Lys	Ser	Trp	Leu	Ala	Glu	Val	Ile	Arg	Phe	Ile	Asn	Asp	Ile	Leu	
		115					120					125				
ctc	tct	gcg	ccg	tcg	att	gtg	gtt	ggc	ctg	ttt	gtt	tac	acc	att	gtg	432
Leu	Ser	Ala	Pro	Ser	Ile	Val	Val	Gly	Leu	Phe	Val	Tyr	Thr	Ile	Val	
			130				135					140				
gtg	gcg	cag	atg	gag	cac	ttc	tcc	ggc	tgg	gcg	ggc	gtg	att	gcc	ctg	480
Val	Ala	Gln	Met	Glu	His	Phe	Ser	Gly	Trp	Ala	Gly	Val	Ile	Ala	Leu	
	145				150					155					160	
gcg	ttg	ttg	cag	gtg	ccg	att	gtt	atc	cgc	acc	acc	gag	aac	atg	ctg	528
Ala	Leu	Leu	Gln	Val	Pro	Ile	Val	Ile	Arg	Thr	Thr	Glu	Asn	Met	Leu	
				165					170					175		
aaa	ctg	gtg	ccg	tac	agc	ctg	cgt	gaa	gcg	gct	tat	gcg	ctg	ggc	aca	576
Lys	Leu	Val	Pro	Tyr	Ser	Leu	Arg	Glu	Ala	Ala	Tyr	Ala	Leu	Gly	Thr	
			180					185					190			
ccg	aag	tgg	aag	atg	atc	tct	gcg	att	acg	ctg	aaa	gcg	tcg	gtg	tcc	624
Pro	Lys	Trp	Lys	Met	Ile	Ser	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Val	Ser	
			195				200					205				
ggg	att	atg	acc	ggc	atc	ctg	ctg	gcg	att	gcc	cgt	att	gct	ggc	gaa	672
Gly	Ile	Met	Thr	Gly	Ile	Leu	Leu	Ala	Ile	Ala	Arg	Ile	Ala	Gly	Glu	
	210					215					220					
acc	gcg	ccg	ctg	ctg	ttt	acc	gcg	ctc	tcc	aac	cag	ttc	tgg	agc	acg	720
Thr	Ala	Pro	Leu	Leu	Phe	Thr	Ala	Leu	Ser	Asn	Gln	Phe	Trp	Ser	Thr	

ggt atc gcc att gag ctg ctg gca gcc att cca agt atc gtt tac ggc	384
Gly Ile Ala Ile Glu Leu Leu Ala Ala Ile Pro Ser Ile Val Tyr Gly	
115 120 125	
atg tgg ggc ctg ttt atc ttt gcg ccg ctg ttc gcc gtt tac ttt cag	432
Met Trp Gly Leu Phe Ile Phe Ala Pro Leu Phe Ala Val Tyr Phe Gln	
130 135 140	
gag ccg gtc ggc aat atc atg tcg aat atc ccg att gtt ggc gcg ctg	480
Glu Pro Val Gly Asn Ile Met Ser Asn Ile Pro Ile Val Gly Ala Leu	
145 150 155 160	
ttc tct ggc ccc gca ttt ggt atc ggt atc ctc gcg gca ggc gtg atc	528
Phe Ser Gly Pro Ala Phe Gly Ile Gly Ile Leu Ala Ala Gly Val Ile	
165 170 175	
ctc gcc atc atg att att ccg tac att gcg gcg gta atg cgt gat gtg	576
Leu Ala Ile Met Ile Ile Pro Tyr Ile Ala Ala Val Met Arg Asp Val	
180 185 190	
ttc gaa caa acc ccg gtg atg atg aaa gag tcg gcc tac ggt att ggc	624
Phe Glu Gln Thr Pro Val Met Met Lys Glu Ser Ala Tyr Gly Ile Gly	
195 200 205	
tgc acc acc tgg gaa gtt atc tgg cgt atc gtt ctt ccg ttc acc aaa	672
Cys Thr Thr Trp Glu Val Ile Trp Arg Ile Val Leu Pro Phe Thr Lys	
210 215 220	
aat ggt gtt atc ggc ggc atc atg ctg ggg ctg ggc cgc gcg ctc ggt	720
Asn Gly Val Ile Gly Gly Ile Met Leu Gly Leu Gly Arg Ala Leu Gly	
225 230 235 240	
gaa acc atg gcg gtg acc ttt atc atc ggt aac acc tac cag ctc gac	768
Glu Thr Met Ala Val Thr Phe Ile Ile Gly Asn Thr Tyr Gln Leu Asp	
245 250 255	
agc gcc tcg ctg tat atg ccg ggc aac agt atc acc tct gcg ctg gcg	816
Ser Ala Ser Leu Tyr Met Pro Gly Asn Ser Ile Thr Ser Ala Leu Ala	
260 265 270	
aac gaa ttt gcg gaa gcg gaa tcc ggt ctg cac gtt gcc gca ctg atg	864
Asn Glu Phe Ala Glu Ala Glu Ser Gly Leu His Val Ala Ala Leu Met	
275 280 285	
gaa ctg ggc ctg atc ctg ttt gtg att acc ttc atc gtc ctc gcc gca	912
Glu Leu Gly Leu Ile Leu Phe Val Ile Thr Phe Ile Val Leu Ala Ala	
290 295 300	
tcg aag ttt atg att atg cgc ctg gct aag aat gag ggg gca cgc taa	960
Ser Lys Phe Met Ile Met Arg Leu Ala Lys Asn Glu Gly Ala Arg *	
305 310 315	

<210> 187
 <211> 1041
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1041)

<400> 187

atg	aaa	ggt	atg	cgt	acc	acc	gtc	gca	act	ggt	gtc	gcc	gcg	acc	tta	48
Met	Lys	Val	Met	Arg	Thr	Thr	Val	Ala	Thr	Val	Val	Ala	Ala	Thr	Leu	
1				5					10					15		
tcg	atg	agt	gct	ttc	tct	gtg	ttt	gca	gaa	gca	agc	ctg	aca	ggt	gca	96
Ser	Met	Ser	Ala	Phe	Ser	Val	Phe	Ala	Glu	Ala	Ser	Leu	Thr	Gly	Ala	
			20					25					30			
ggt	gca	acc	ttc	cct	gcg	ccg	gtg	tat	gcc	aaa	tgg	gct	gac	act	tac	144
Gly	Ala	Thr	Phe	Pro	Ala	Pro	Val	Tyr	Ala	Lys	Trp	Ala	Asp	Thr	Tyr	
		35					40					45				
cag	aaa	gaa	acc	ggt	aat	aaa	ggt	aac	tac	cag	ggt	atc	ggt	tct	tcc	192
Gln	Lys	Glu	Thr	Gly	Asn	Lys	Val	Asn	Tyr	Gln	Gly	Ile	Gly	Ser	Ser	
	50					55					60					
ggt	ggc	gta	aaa	cag	att	atc	gct	aat	acc	ggt	gat	ttt	ggt	gcc	tct	240
Gly	Gly	Val	Lys	Gln	Ile	Ile	Ala	Asn	Thr	Val	Asp	Phe	Gly	Ala	Ser	
65					70					75					80	
gac	gcg	ccg	ctg	tct	gac	gaa	aaa	ctg	gct	cag	gaa	ggt	ctg	ttc	cag	288
Asp	Ala	Pro	Leu	Ser	Asp	Glu	Lys	Leu	Ala	Gln	Glu	Gly	Leu	Phe	Gln	
				85					90					95		
ttc	ccg	acc	gtg	att	ggc	ggc	gtg	gtg	ctg	gcg	ggt	aac	att	cca	ggg	336
Phe	Pro	Thr	Val	Ile	Gly	Gly	Val	Val	Leu	Ala	Val	Asn	Ile	Pro	Gly	
			100					105					110			
ctg	aag	tct	ggc	gaa	ctg	gtg	ctg	gat	ggt	aaa	acc	ctc	ggc	gac	atc	384
Leu	Lys	Ser	Gly	Glu	Leu	Val	Leu	Asp	Gly	Lys	Thr	Leu	Gly	Asp	Ile	
		115					120					125				
tac	ctg	ggc	aaa	atc	aag	aag	tgg	gat	gat	gaa	gcc	atc	gcc	aaa	ctg	432
Tyr	Leu	Gly	Lys	Ile	Lys	Lys	Trp	Asp	Asp	Glu	Ala	Ile	Ala	Lys	Leu	
	130					135					140					
aat	ccg	ggt	ctg	aaa	ctg	cct	tca	caa	aac	att	gct	gta	gta	cgc	cgc	480
Asn	Pro	Gly	Leu	Lys	Leu	Pro	Ser	Gln	Asn	Ile	Ala	Val	Val	Arg	Arg	
145					150					155					160	
gca	gat	ggc	tcc	ggg	act	tcc	ttc	gtc	ttc	acc	agc	tac	ctg	gcg	aaa	528
Ala	Asp	Gly	Ser	Gly	Thr	Ser	Phe	Val	Phe	Thr	Ser	Tyr	Leu	Ala	Lys	
				165					170					175		
gtg	aac	gaa	gag	tgg	aaa	aac	aac	ggt	ggt	act	ggc	tct	acc	gta	aaa	576
Val	Asn	Glu	Glu	Trp	Lys	Asn	Asn	Val	Gly	Thr	Gly	Ser	Thr	Val	Lys	
			180					185					190			
tgg	ccg	atc	ggt	ctg	ggc	ggt	aaa	ggt	aac	gac	ggt	atc	gcc	gcg	ttc	624
Trp	Pro	Ile	Gly	Leu	Gly	Gly	Lys	Gly	Asn	Asp	Gly	Ile	Ala	Ala	Phe	

caa tgt gta aaa aaa agc cgt ggc cgc cca aaa gtg ttc gac agg gat	144
Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp	
35 40 45	
gcc gcg ctt gat aag gcc atg aaa ttg ttc tgg caa cac ggt tat gaa	192
Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu	
50 55 60	
gcg act tct ctt gcg gac ctc gtc gaa gcg acc gga gcc aaa gcg ccc	240
Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro	
65 70 75 80	
acg cta tac gcg gaa ttt acc aac aaa gag ggg tta ttt cgt gcc gtt	288
Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val	
85 90 95	
ctc gac cgc tat atc gat cgt ttt gcc gct aag cat gaa gca cag ctg	336
Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu	
100 105 110	
ttt tgt gaa gag aaa agc gtg gag tct gcg ctg gct gac tat ttt gct	384
Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala	
115 120 125	
gcc atc gcc aac tgc ttt acc agc aaa gac acc ccg gca ggc tgc ttc	432
Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe	
130 135 140	
atg atc aac aac tgc acc acc ctc tcc cca gat tca gga gat atc gcc	480
Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala	
145 150 155 160	
aat acg ttg aaa tca cgc cat gcg atg caa gag cgc act ttg cag cag	528
Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln	
165 170 175	
ttt tta tgt caa cga caa gcg cgc ggg gaa atc ccg ccc cac tgt gac	576
Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp	
180 185 190	
gtg aca cat ctg gca gaa ttc ctt aat tgt att att cag ggg atg tcg	624
Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser	
195 200 205	
atc agc gca cgc gaa ggt gca tcg ctg gaa aaa ctg atg cag att gcc	672
Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala	
210 215 220	
gga acg act ttg cgt tta tgg ccc gaa ctg gtg aaa taa	711
Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys *	
225 230 235	

<210> 189
 <211> 546
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(546)

<400> 189

gtg	cag	gcc	aaa	att	gcg	gca	tca	aat	acg	ggg	gaa	ctg	gat	gcc	ctg	48
Met	Gln	Ala	Lys	Ile	Ala	Ala	Ser	Asn	Thr	Gly	Glu	Leu	Asp	Ala	Leu	
1				5					10					15		
caa	cag	ctg	gga	ttc	tcc	ctg	gta	gaa	ggg	gaa	gtt	gat	ttg	gcg	cta	96
Gln	Gln	Leu	Gly	Phe	Ser	Leu	Val	Glu	Gly	Glu	Val	Asp	Leu	Ala	Leu	
		20						25					30			
ccc	gtg	aac	aat	gcc	agt	gat	agc	ggg	gct	gta	gtg	gca	caa	gag	acc	144
Pro	Val	Asn	Asn	Ala	Ser	Asp	Ser	Gly	Ala	Val	Val	Ala	Gln	Glu	Thr	
		35					40					45				
gat	att	ccc	gca	tta	cgt	cag	tta	gcc	agc	gcc	gca	ttt	gcg	caa	agc	192
Asp	Ile	Pro	Ala	Leu	Arg	Gln	Leu	Ala	Ser	Ala	Ala	Phe	Ala	Gln	Ser	
	50					55					60					
cgt	ttt	cgt	gcg	ccg	tgg	tat	gcg	cct	gac	gcc	agc	agt	cgc	ttt	tat	240
Arg	Phe	Arg	Ala	Pro	Trp	Tyr	Ala	Pro	Asp	Ala	Ser	Ser	Arg	Phe	Tyr	
65					70				75					80		
gca	cag	tgg	att	gaa	aat	gcc	gtg	cgc	ggc	acc	ttt	gat	cat	caa	tgt	288
Ala	Gln	Trp	Ile	Glu	Asn	Ala	Val	Arg	Gly	Thr	Phe	Asp	His	Gln	Cys	
			85					90						95		
ctg	att	tta	cgt	gcg	gcg	tcc	ggc	gat	att	cgc	ggc	tat	gtc	tct	tta	336
Leu	Ile	Leu	Arg	Ala	Ala	Ser	Gly	Asp	Ile	Arg	Gly	Tyr	Val	Ser	Leu	
			100					105					110			
cgg	gaa	ctc	aat	gcg	aca	gat	gcg	cga	att	ggc	ctg	ctg	gct	gga	cgc	384
Arg	Glu	Leu	Asn	Ala	Thr	Asp	Ala	Arg	Ile	Gly	Leu	Leu	Ala	Gly	Arg	
		115					120					125				
ggg	gca	ggg	gct	gag	ctg	atg	caa	acg	gcg	cta	aac	tgg	gcg	tat	cgt	432
Gly	Ala	Gly	Ala	Glu	Leu	Met	Gln	Thr	Ala	Leu	Asn	Trp	Ala	Tyr	Arg	
	130					135					140					
cgc	ggg	aaa	aca	act	ttg	cgg	gtg	gcg	acc	caa	atg	ggc	aac	acc	gcc	480
Arg	Gly	Lys	Thr	Thr	Leu	Arg	Val	Ala	Thr	Gln	Met	Gly	Asn	Thr	Ala	
145					150					155					160	
gcg	ctt	aaa	cga	tac	ata	caa	agt	ggg	gcg	aat	gta	gaa	agc	acc	gcg	528
Ala	Leu	Lys	Arg	Tyr	Ile	Gln	Ser	Gly	Ala	Asn	Val	Glu	Ser	Thr	Ala	
				165					170					175		
tac	tgg	tta	tac	agg	tga											546
Tyr	Trp	Leu	Tyr	Arg	*											
			180													

<210> 190
 <211> 1131

<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1131)

<400> 190

atg att cca ttt aac gca ccg ccg gtg gtg gga acc gaa ctc gac tat	48
Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr	
1 5 10 15	
atg cag tcg gca atg ggt agc ggc aaa ctg tgt ggc gat ggc ggt ttt	96
Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe	
20 25 30	
acc cgt cgc tgc cag cag tgg ctg gag caa cgt ttt ggc agc gcc aaa	144
Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys	
35 40 45	
gtg tta ctg acg ccg tcc tgc acc gct tcg ctg gag atg gcg gcg ctg	192
Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu	
50 55 60	
ctg ctc gat atc cag cct ggc gat gaa gtg atc atg ccg agc tac acc	240
Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr	
65 70 75 80	
ttt gtc tcc acc gcc aat gcc ttt gtg ctg cgt ggc gca aaa atc gtt	288
Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val	
85 90 95	
ttt gtg gat gtt cgc ccg gac acc atg aac atc gac gaa acg ctg att	336
Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile	
100 105 110	
gaa gcg gcg atc acc gac aaa acg cgc gtt atc gtg ccg gtc cat tac	384
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr	
115 120 125	
gcg ggt gtg gcc tgc gaa atg gac acc att atg gcg ttg gcg aaa aag	432
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys	
130 135 140	
cat aat ttg ttt gtg gta gaa gat gcc gct cag ggc gtg atg tcc act	480
His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr	
145 150 155 160	
tac aaa ggg cgt gca ctg gga acc att ggt cat att ggc tgc ttt agc	528
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser	
165 170 175	
ttc cat gaa acc aaa aac tac acg gcg ggc ggt gaa ggc ggc gcg acg	576
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr	
180 185 190	
ctg att aac gat aaa gcg tta atc gaa cga gcc gag atc atc cgt gaa	624

<220>
 <221> CDS
 <222> (1)...(1353)

<400> 192

atg agt ctg ctg caa ttc agt ggc ctg ttt gtt gtc tgg ctg ctc tgc	48
Met Ser Leu Leu Gln Phe Ser Gly Leu Phe Val Val Trp Leu Leu Cys	
1 5 10 15	
acg ctg ttt att gcc acg ctg acc tgg ttt gag ttt cgc cgt gtg cgc	96
Thr Leu Phe Ile Ala Thr Leu Thr Trp Phe Glu Phe Arg Arg Val Arg	
20 25 30	
ttt aac ttc aat gtc ttc ttt tca ttg ctg ttt ttg ctc acc ttt ttc	144
Phe Asn Phe Asn Val Phe Phe Ser Leu Leu Phe Leu Leu Thr Phe Phe	
35 40 45	
ttc ggc ttc ccg ctg acc agc gtg ctg gta ttt cgc ttt gat gtt ggt	192
Phe Gly Phe Pro Leu Thr Ser Val Leu Val Phe Arg Phe Asp Val Gly	
50 55 60	
gtc gcg ccg cca gaa atc ttg ttg cag gcg ttg ctt tct gcg ggc tgc	240
Val Ala Pro Pro Glu Ile Leu Leu Gln Ala Leu Leu Ser Ala Gly Cys	
65 70 75 80	
ttc tac gcg gtt tac tat gtc acc tac aaa acc cgc cta cgc aaa cgc	288
Phe Tyr Ala Val Tyr Tyr Val Thr Tyr Lys Thr Arg Leu Arg Lys Arg	
85 90 95	
gtt gct gat gta ccg cgc cgt ccg ctg ttt acc atg aac cgc gtg gag	336
Val Ala Asp Val Pro Arg Arg Pro Leu Phe Thr Met Asn Arg Val Glu	
100 105 110	
acc aat ctt acg tgg gtg atc ctg atg ggt atc gcg ctg gta agc gtc	384
Thr Asn Leu Thr Trp Val Ile Leu Met Gly Ile Ala Leu Val Ser Val	
115 120 125	
ggc atc ttc ttc atg cac aac ggc ttt ttg ctg ttc cgg ctt aac tcc	432
Gly Ile Phe Phe Met His Asn Gly Phe Leu Leu Phe Arg Leu Asn Ser	
130 135 140	
tac agt cag atc ttt tcc agt gaa gtc tcc ggc gtg gcg tta aaa cgc	480
Tyr Ser Gln Ile Phe Ser Ser Glu Val Ser Gly Val Ala Leu Lys Arg	
145 150 155 160	
ttc ttt tac ttt ttc atc ccg gcg atg ctg gtg gtc tac ttt ctg cgc	528
Phe Phe Tyr Phe Phe Ile Pro Ala Met Leu Val Val Tyr Phe Leu Arg	
165 170 175	
cag gac agc aaa gcg tgg ctg ttt ttc ctc gtc agc acg gtc gcc ttt	576
Gln Asp Ser Lys Ala Trp Leu Phe Phe Leu Val Ser Thr Val Ala Phe	
180 185 190	
ggc ttg ctg act tat atg att gtc ggc ggc act cgc gcc aat atc atc	624
Gly Leu Leu Thr Tyr Met Ile Val Gly Gly Thr Arg Ala Asn Ile Ile	
195 200 205	

gcc gga ctc att cat aaa cgt aca aaa tca tcg ctc cgg acg cag gtt 1344
 Ala Gly Leu Ile His Lys Arg Thr Lys Ser Ser Leu Arg Thr Gln Val
 435 440 445

gaa gga taa 1353
 Glu Gly *
 450

<210> 193
 <211> 741
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(741)

<400> 193
 atg aat aac aac acc acg gca cca acc tat acg ctg cgt ggc tta cag 48
 Met Asn Asn Asn Thr Thr Ala Pro Thr Tyr Thr Leu Arg Gly Leu Gln
 1 5 10 15

ttg att ggt tgg cgt gat atg cag cac gcc ctc gat tat ctg ttt gct 96
 Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Tyr Leu Phe Ala
 20 25 30

gac ggg cag ctt aag cag gga acg ctg gtt gcc att aat gct gaa aaa 144
 Asp Gly Gln Leu Lys Gln Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
 35 40 45

atg ctg act att gaa gat aac gcc gag gtc agg gag tta att aac gct 192
 Met Leu Thr Ile Glu Asp Asn Ala Glu Val Arg Glu Leu Ile Asn Ala
 50 55 60

gcc gaa ttt aaa tat gcg gat ggc atc agc gtt gta cgt tca gta cgt 240
 Ala Glu Phe Lys Tyr Ala Asp Gly Ile Ser Val Val Arg Ser Val Arg
 65 70 75 80

aaa aag tac ccg cag gcg cag gtt tcc cgc gtt gcc ggt gcc gat ctc 288
 Lys Lys Tyr Pro Gln Ala Gln Val Ser Arg Val Ala Gly Ala Asp Leu
 85 90 95

tgg gaa gag ctg atg gcg cgc gca ggc aaa gaa ggg acg ccg gta ttt 336
 Trp Glu Glu Leu Met Ala Arg Ala Gly Lys Glu Gly Thr Pro Val Phe
 100 105 110

ctt gtg ggc ggt aaa cct gaa gtg ctg gcg caa act gaa gct aaa ctg 384
 Leu Val Gly Gly Lys Pro Glu Val Leu Ala Gln Thr Glu Ala Lys Leu
 115 120 125

cgc aac cag tgg aat gtg aat atc gtt ggc agt cag gat ggt tat ttt 432
 Arg Asn Gln Trp Asn Val Asn Ile Val Gly Ser Gln Asp Gly Tyr Phe
 130 135 140

aaa ccc gag cag cgt cag gcg ctg ttt gaa cgc att cat gcc agc ggt 480
 Lys Pro Glu Gln Arg Gln Ala Leu Phe Glu Arg Ile His Ala Ser Gly

<210> 195
 <211> 615
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(615)

<400> 195
 gtg cgg ggc gaa ctg ctg ttc ttc ccg acg cgg atg gac cct tcg ctc 48
 Met Arg Gly Glu Leu Leu Phe Phe Pro Thr Arg Met Asp Pro Ser Leu
 1 5 10 15
 aat acg atg gcg aac gat cgg caa cgt gaa ggg aaa atg acc att ctg 96
 Asn Thr Met Ala Asn Asp Arg Gln Arg Glu Gly Lys Met Thr Ile Leu
 20 25 30
 gtg ggg aac tcc ggc gac cgc agc aat gag cat att gct gcc ttg cgc 144
 Val Gly Asn Ser Gly Asp Arg Ser Asn Glu His Ile Ala Ala Leu Arg
 35 40 45
 gcc gtt cat cag caa ttt ggc gat acg gta aaa gtg gtg gtg ccg atg 192
 Ala Val His Gln Gln Phe Gly Asp Thr Val Lys Val Val Val Pro Met
 50 55 60
 gga tat ccg cct aat aac gaa gcg tac att gag gaa gtt cgt cag gcg 240
 Gly Tyr Pro Pro Asn Asn Glu Ala Tyr Ile Glu Glu Val Arg Gln Ala
 65 70 75 80
 ggg ctg gag tta ttc agc gaa gaa aat cta caa att ctg agc gaa aaa 288
 Gly Leu Glu Leu Phe Ser Glu Glu Asn Leu Gln Ile Leu Ser Glu Lys
 85 90 95
 ctg gaa ttt gac gcc tat ctg gcg cta ctt cgt cag tgc gat ctt ggt 336
 Leu Glu Phe Asp Ala Tyr Leu Ala Leu Leu Arg Gln Cys Asp Leu Gly
 100 105 110
 tac ttt att ttt gcc cgc cag cag ggc att ggt acg ctg tgc tta ctg 384
 Tyr Phe Ile Phe Ala Arg Gln Gln Gly Ile Gly Thr Leu Cys Leu Leu
 115 120 125
 att cag gcg ggc att cct tgt gtg ctt aac cgg gaa aat ccg ttc tgg 432
 Ile Gln Ala Gly Ile Pro Cys Val Leu Asn Arg Glu Asn Pro Phe Trp
 130 135 140
 cag gat atg acg gaa caa cat ttg ccg gtg ctg ttt act acc gac gat 480
 Gln Asp Met Thr Glu Gln His Leu Pro Val Leu Phe Thr Thr Asp Asp
 145 150 155 160
 ctc aac gag gat att gtg cgt gaa gcg cag cgc cag ttg gcg tcg gtg 528
 Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
 165 170 175
 gat aaa aac acc att gcc ttc ttt agc cct aac tat cta caa ggc tgg 576
 Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp

180

185

190

cag cgg gcg ttg gcg att gcc gcc agg gag gtc gca tga
 Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala *
 195 200

615

<210> 196

<211> 549

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(549)

<400> 196

atg att cgg caa cgt cgt cgt gcg tta acg ccg gaa caa cag cag gaa 48
 Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
 1 5 10 15

atg ggt caa caa gcc gct acc cgg atg atg act tat ccc ccg gtg gtg 96
 Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
 20 25 30

atg gca cat acg gtc gct gta ttc ctc tct ttt gat ggc gaa ctc gac 144
 Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
 35 40 45

acc cag cca ctc ata gaa caa ctc tgg cgc gcc ggt aag cgc gta tat 192
 Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
 50 55 60

ctt cca gtt ttg cat ccc ttt agt gcc ggt aat ttg ctg ttc ctg aat 240
 Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
 65 70 75 80

tac cat ccg caa agc gaa ctg gtg atg aac agg ttg aag atc cat gag 288
 Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
 85 90 95

cca aaa ttg gat gtg cgt gac gtg cta ccc ctt tcc cga tta gac gtg 336
 Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
 100 105 110

ctg atc aca ccg ctg gtc gcc ttt gat gag tac ggt cag cgc ctg gga 384
 Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
 115 120 125

atg ggc ggt ggt ttt tat gat cgg acc tta caa aac tgg cag cac tat 432
 Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
 130 135 140

aaa acg caa ccg gtg ggt tat gcg cat gat tgt cag ttg gtg gaa aaa 480
 Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
 145 150 155 160

CCDS:CCDS1461.1

ctc ccc gtt gaa gag tgg gat atc cct ctt cct gcg gtg gtt aca ccg 528
 Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
 165 170 175

tcg aaa gtc tgg gag tgg taa 549
 Ser Lys Val Trp Glu Trp *
 180

<210> 197
 <211> 276
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(276)

<400> 197
 atg gca cgc gta act gtt cag gac gct gta gag aaa att ggt aac cgt 48
 Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
 1 5 10 15
 ttt gac ctg gta ctg gtc gcc gcg cgt cgc gct cgt cag atg cag gta 96
 Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
 20 25 30
 ggc gga aag gat ccg ctg gta ccg gaa gaa aac gat aaa acc act gta 144
 Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
 35 40 45
 atc gcg ctg cgc gaa atc gaa gaa ggt ctg atc aac aac cag atc ctc 192
 Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
 50 55 60
 gac gtt cgc gaa cgc cag gaa cag caa gag cag gaa gcc gct gaa tta 240
 Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu
 65 70 75 80
 caa gcc gtt acc gct att gct gaa ggt cgt cgt taa 276
 Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg *
 85 90

<210> 198
 <211> 2109
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2109)

<400> 198
 ttg tat ctg ttt gaa agc ctg aat caa ctg att caa acc tac ctg ccg 48
 Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro
 1 5 10 15

gaa gac caa atc aag cgt ctg cgg cag gcg tat ctc gtt gca cgt gat Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp																	96
202530																	
gct cac gag ggg caa aca cgt tca agc ggt gaa ccc tat atc acg cac Ala His Glu Gly Gln Thr Arg Ser Ser Gly Glu Pro Tyr Ile Thr His																	144
354045																	
ccg gta gcg gtt gcc tgc att ctg gcc gag atg aaa ctc gac tat gaa Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu																	192
505560																	
acg ctg atg gcg gcg ctg ctg cat gac gtg att gaa gat act ccc gcc Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala																	240
65707580																	
acc tac cag gat atg gaa cag ctt ttt ggt aaa agc gtc gcc gag ctg Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu																	288
859095																	
gta gag ggg gtg tcg aaa ctt gat aaa ctc aag ttc cgc gat aag aaa Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys																	336
100105110																	
gag gcg cag gcc gaa aac ttt cgc aag atg att atg gcg atg gtg cag Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln																	384
115120125																	
gat atc cgc gtc atc ctc atc aaa ctt gcc gac cgt acc cac aac atg Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met																	432
130135140																	
cgc acg ctg ggc tca ctt cgc ccg gac aaa cgt cgc cgc atc gcc cgt Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg																	480
145150155160																	
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165170175																	
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180185190																	
aac cgt tat cgc gta atc aaa gaa gtg gtg aaa gcc gcg cgc ggc aac Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn																	624
195200205																	
cgt aaa gag atg atc cag aag att ctt tct gaa atc gaa ggg cgt ttg Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu																	672
210215220																	
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 Gln Pro Asp Leu Thr Val Cys Met Glu Gln Val His Lys Pro His Asn
 20 25 30
 gtt tct gcg att att cgt acc gca gat gcc gtt ggc gta cat gaa gtt 144
 Val Ser Ala Ile Ile Arg Thr Ala Asp Ala Val Gly Val His Glu Val
 35 40 45
 cac gcc gtc tgg cct ggt agc cgc atg cgc acc atg gct tcg gca gcg 192
 His Ala Val Trp Pro Gly Ser Arg Met Arg Thr Met Ala Ser Ala Ala
 50 55 60
 gcg ggt agt aac agc tgg gta cag gtg aaa aca cac cgc acc att ggc 240
 Ala Gly Ser Asn Ser Trp Val Gln Val Lys Thr His Arg Thr Ile Gly
 65 70 75 80
 gat gcc gtc gct cat ctc aaa ggc cag ggc atg cag att ctg gca acc 288
 Asp Ala Val Ala His Leu Lys Gly Gln Gly Met Gln Ile Leu Ala Thr
 85 90 95
 cat ctt tct gat aac gct gtc gat ttc cgc gaa att gat tac act cgc 336
 His Leu Ser Asp Asn Ala Val Asp Phe Arg Glu Ile Asp Tyr Thr Arg
 100 105 110
 ccg acc tgc att ttg atg gga cag gag aaa acg ggc atc acg cag gaa 384
 Pro Thr Cys Ile Leu Met Gly Gln Glu Lys Thr Gly Ile Thr Gln Glu
 115 120 125
 gca ttg gcc ctg gcg gat cag gac atc atc att ccg atg atc ggc atg 432
 Ala Leu Ala Leu Ala Asp Gln Asp Ile Ile Ile Pro Met Ile Gly Met
 130 135 140
 gtg cag tcg ctg aat gtt tcc gtt gcc tca gcc ctc att ctt tac gaa 480
 Val Gln Ser Leu Asn Val Ser Val Ala Ser Ala Leu Ile Leu Tyr Glu
 145 150 155 160
 gcc cag cgt cag cgg caa aat gca ggc atg tac ctg cgt gaa aac agc 528
 Ala Gln Arg Gln Arg Gln Asn Ala Gly Met Tyr Leu Arg Glu Asn Ser
 165 170 175

atg ttg ccg gaa gca gag caa caa cgc ctg ttg ttt gaa ggc ggc tat	576
Met Leu Pro Glu Ala Glu Gln Gln Arg Leu Leu Phe Glu Gly Gly Tyr	
180 185 190	
ccg gtg ctg gcg aaa gtc gca aaa cgc aaa ggc ctg cct tat ccc cac	624
Pro Val Leu Ala Lys Val Ala Lys Arg Lys Gly Leu Pro Tyr Pro His	
195 200 205	
gtc aat cag caa ggc gag atc gaa gct gat gcc gac tgg tgg gct act	672
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gtt ggc gca gca ctt agt aac aaa ctg gcg aaa atc aac ctg cat acc	96
Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr	
20 25 30	
gtg cag gat cta ctc tta cac ctt ccc ctg cgc tac gaa gat cgc acc	144
Val Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr	
35 40 45	
cat ctc tac ccc atc gga gaa cta ctg ccg ggc gtt tat gcc acg gtg	192
His Leu Tyr Pro Ile Gly Glu Leu Leu Pro Gly Val Tyr Ala Thr Val	
50 55 60	
gaa ggc gaa gtg ctg aac tgc aat atc tcc ttc ggc ggt cgg cgg atg	240
Glu Gly Glu Val Leu Asn Cys Asn Ile Ser Phe Gly Gly Arg Arg Met	
65 70 75 80	
atg acc tgc cag atc agc gac ggt tcc ggc atc ctc acc atg cgc ttt	288
Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Ile Leu Thr Met Arg Phe	
85 90 95	
ttc aat ttc agc gcg gca atg aaa aat agc ctg gcg gcg ggc cgc cgt	336
Phe Asn Phe Ser Ala Ala Met Lys Asn Ser Leu Ala Ala Gly Arg Arg	
100 105 110	
gta ctg gct tat ggc gaa gca aag cgc ggt aaa tat ggt gcg gag atg	384

340				345				350								
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Gly	Lys	Gln	Lys	Gly	Lys	Ala	Arg	Leu	Ala	Gln	Gln	Glu	Ala	Ile	Ala	
355				360				365								
agc	ggt	cag	gtg	cag	atg	att	gtc	ggt	aca	cac	gcc	atc	ttc	cag	gaa	1152
Ser	Gly	Gln	Val	Gln	Met	Ile	Val	Gly	Thr	His	Ala	Ile	Phe	Gln	Glu	
370				375				380								
cag	gtg	cag	ttt	aac	ggc	ctg	gcg	ctg	gtg	att	atc	gac	gaa	cag	cat	1200
Gln	Val	Gln	Phe	Asn	Gly	Leu	Ala	Leu	Val	Ile	Ile	Asp	Glu	Gln	His	
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cgt	ttt	ggc	gtg	cat	cag	cgt	ctg	gca	ttg	tgg	gag	aaa	ggc	cag	cag	1248
Arg	Phe	Gly	Val	His	Gln	Arg	Leu	Ala	Leu	Trp	Glu	Lys	Gly	Gln	Gln	
405				410				415								
cag	ggc	ttc	cat	ccg	cat	cag	ttg	atc	atg	acc	gcc	acg	ccg	atc	ccc	1296
Gln	Gly	Phe	His	Pro	His	Gln	Leu	Ile	Met	Thr	Ala	Thr	Pro	Ile	Pro	
420				425				430								
cgc	acg	ctg	gca	atg	act	gcg	tat	gcc	gat	ctc	gat	acc	tcg	gtg	ata	1344
Arg	Thr	Leu	Ala	Met	Thr	Ala	Tyr	Ala	Asp	Leu	Asp	Thr	Ser	Val	Ile	
435				440				445								
gat	gag	ctg	ccg	cca	ggc	cgc	acg	cca	gtg	act	acg	gtc	gct	att	cct	1392
Asp	Glu	Leu	Pro	Pro	Gly	Arg	Thr	Pro	Val	Thr	Thr	Val	Ala	Ile	Pro	
450				455				460								
gat	acc	cgc	cgt	acc	gac	atc	att	gac	cgc	gtg	cac	cac	gcc	tgc	ata	1440
Asp	Thr	Arg	Arg	Thr	Asp	Ile	Ile	Asp	Arg	Val	His	His	Ala	Cys	Ile	
465				470				475				480				
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Thr	Glu	Gly	Arg	Gln	Ala	Tyr	Trp	Val	Cys	Thr	Leu	Ile	Glu	Glu	Ser	
485				490				495								
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Glu	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Glu	Ala	Thr	Trp	Glu	Glu	Leu	Lys	
500				505				510								
ctg	gcg	cta	cca	gag	ttg	aac	gtt	ggc	ctg	gta	cac	ggg	cgg	atg	aaa	1584
Leu	Ala	Leu	Pro	Glu	Leu	Asn	Val	Gly	Leu	Val	His	Gly	Arg	Met	Lys	
515				520				525								
cct	gcc	gag	aaa	cag	gcg	gtg	atg	gcg	tcg	ttt	aaa	caa	ggt	gag	cta	1632
Pro	Ala	Glu	Lys	Gln	Ala	Val	Met	Ala	Ser	Phe	Lys	Gln	Gly	Glu	Leu	
530				535				540								
cac	ctg	ctg	gtt	gcc	aca	acc	gtt	att	gaa	gtc	ggc	gtt	gat	gtg	cct	1680
His	Leu	Leu	Val	Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Val	Asp	Val	Pro	
545				550				555				560				
aac	gcc	agt	ctg	atg	att	atc	gaa	aac	ccg	gag	cgt	ctg	ggt	ctg	gcg	1728
Asn	Ala	Ser	Leu	Met	Ile	Ile	Glu	Asn	Pro	Glu	Arg	Leu	Gly	Leu	Ala	
565				570				575								

cag tta cac cag ctg cgc ggg cgc gta ggt cgt ggc gcg gtg gct tct 1776
Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
580 585 590

cac tgc gtg ctg ctc tac aaa acg ccg ctt tct aaa acg gcg caa att 1824
His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Ile
595 600 605

cgc ctg caa gtg ctg cgc gac agt aac gac ggt ttt gtg att gcg caa 1872
Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
610 615 620

aaa gat ctg gag att cgc ggc cct ggc gaa ttg tta ggc acg cgt cag 1920
Lys Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
625 630 635 640

acg ggt aat gct gaa ttt aaa gtg gcg gat tta ctg cgc gat cag gcg 1968
Thr Gly Asn Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
645 650 655

atg atc ccg gaa gtt cag cgc ctg gca cgc cat att cac gaa cgt tac 2016
Met Ile Pro Glu Val Gln Arg Leu Ala Arg His Ile His Glu Arg Tyr
660 665 670

cca caa cag gca aaa gcc ctg ata gaa cgc tgg atg ccg gag acg gaa 2064
Pro Gln Gln Ala Lys Ala Leu Ile Glu Arg Trp Met Pro Glu Thr Glu
675 680 685

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ata gcc att ggt att ctc ctt ggc cat ttc tat cct gaa ata ggc gag 96
Ile Ala Ile Gly Ile Leu Leu Gly His Phe Tyr Pro Glu Ile Gly Glu
20 25 30

caa atg aaa ccg ctt ggc gac ggc ttc gtt aag ctc att aag atg atc 144
Gln Met Lys Pro Leu Gly Asp Gly Phe Val Lys Leu Ile Lys Met Ile
35 40 45

atc gct cct gtc atc ttt tgt acc gtc gta acg ggc att gcg ggc atg 192

Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met	
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Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr	
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Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val	
				85					90					95		
aac	gtc	gtg	cag	cct	ggt	gcc	gga	atg	aac	gtc	gat	ccg	gca	acg	ctt	336
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu	
			100					105					110			
gat	gcg	aaa	gcg	gta	gcg	gtt	tac	gcc	gat	cag	gcg	aaa	gac	cag	ggc	384
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly	
		115					120					125				
att	gtc	gcc	ttc	att	atg	gat	gtc	atc	ccg	gcg	agc	gtc	att	ggc	gca	432
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala	
	130					135					140					
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Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe	
145					150					155					160	
ggt	ttt	gcg	ctc	cac	cgt	ctg	ggc	agc	aaa	ggc	caa	ctg	att	ttt	aac	528
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn	
				165					170					175		
gtc	atc	gaa	agt	ttc	tcg	cag	gtc	atc	ttc	ggc	atc	atc	aat	atg	atc	576
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile	
			180					185					190			
atg	cgt	ctg	gca	cct	att	ggt	gcg	ttc	ggg	gca	atg	gcg	ttt	acc	atc	624
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile	
		195					200					205				
ggt	aaa	tac	ggc	gtc	ggc	aca	ctg	gtg	caa	ctg	ggg	cag	ctg	att	atc	672
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile	
	210					215					220					
tgt	ttc	tac	att	acc	tgt	atc	ctg	ttt	gtg	gtg	ctg	gta	ttg	ggt	tca	720
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser	
225					230					235					240	
atc	gct	aaa	gcg	act	ggt	ttc	agt	atc	ttc	aaa	ttt	atc	cgc	tac	atc	768
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile	
				245					250					255		
cgt	gaa	gaa	ctg	ctg	att	gta	ctg	ggg	act	tca	tct	tcc	gag	tcg	gcg	816
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu									

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Tyr Asp Gly Asn Pro Leu Ala Gln Gln His Gly Pro Arg Tyr Phe Met	
50 55 60	
ctc aat aag cct cag ggc tat gtt tgc tcc acg gac gac cct gat cac	240
Leu Asn Lys Pro Gln Gly Tyr Val Cys Ser Thr Asp Asp Pro Asp His	
65 70 75 80	
cca acg gtg ctc tat ttt ctt gat gaa ccg gta gcg tgg aaa ctg cat	288
Pro Thr Val Leu Tyr Phe Leu Asp Glu Pro Val Ala Trp Lys Leu His	
85 90 95	
gcg gcg ggg cgg ttg gat att gat acc acc ggt ctg gtg ctg atg act	336
Ala Ala Gly Arg Leu Asp Ile Asp Thr Thr Gly Leu Val Leu Met Thr	
100 105 110	
gat gat ggt cag tgg tcg cac cgc att act tct ccg cgc cat cat tgc	384
Asp Asp Gly Gln Trp Ser His Arg Ile Thr Ser Pro Arg His His Cys	
115 120 125	
gag aag acc tat ctg gtg aca ctg gaa tca cct gta gct gac gat acg	432
Glu Lys Thr Tyr Leu Val Thr Leu Glu Ser Pro Val Ala Asp Asp Thr	
130 135 140	
gca gag caa ttt gct aaa ggc gtg cag ctg cat aac gaa aaa gat ctc	480
Ala Glu Gln Phe Ala Lys Gly Val Gln Leu His Asn Glu Lys Asp Leu	
145 150 155 160	
act aag cct gcg gtg ctg gaa gtg att acc cca acg cag gtt cgt ctg	528
Thr Lys Pro Ala Val Leu Glu Val Ile Thr Pro Thr Gln Val Arg Leu	
165 170 175	
acc atc agc gaa ggg cgt tat cat cag gtg aaa cgc atg ttc gcc gcc	576
Thr Ile Ser Glu Gly Arg Tyr His Gln Val Lys Arg Met Phe Ala Ala	
180 185 190	
gtg ggt aac cac gtg gtt gag ctg cat cgt gaa cgt att ggc ggt att	624
Val Gly Asn His Val Val Glu Leu His Arg Glu Arg Ile Gly Gly Ile	
195 200 205	
acg ctg gat gct gat tta gcc ccc ggt gaa tat cgt ccg tta act gaa	672
Thr Leu Asp Ala Asp Leu Ala Pro Gly Glu Tyr Arg Pro Leu Thr Glu	
210 215 220	
gaa gaa att gcc agc gtc gtc taa	696
Glu Glu Ile Ala Ser Val Val *	
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<213> Escherichia coli

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cag	ggg	tat	atc	gac	ctg	tct	gat	ttg	gat	tta	aca	agt	tgt	cat	ttt	96
Gln	Gly	Tyr	Ile	Asp	Leu	Ser	Asp	Leu	Asp	Leu	Thr	Ser	Cys	His	Phe	
			20					25						30		
aaa	ggg	gac	gtt	ata	tcg	aag	gtg	tct	ttt	tta	tca	tca	aat	cta	caa	144
Lys	Gly	Asp	Val	Ile	Ser	Lys	Val	Ser	Phe	Leu	Ser	Ser	Asn	Leu	Gln	
		35					40						45			
cat	gta	aca	ttc	gaa	tgt	aaa	gaa	att	ggg	gat	tgc	aat	ttt	act	act	192
His	Val	Thr	Phe	Glu	Cys	Lys	Glu	Ile	Gly	Asp	Cys	Asn	Phe	Thr	Thr	
	50					55						60				
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Ala	Ile	Val	Asp	Asn	Val	Ile	Phe	Arg	Cys	Arg	Arg	Leu	His	Asn	Val	
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Ile	Phe	Ile	Lys	Ala	Ser	Gly	Glu	Cys	Val	Asp	Phe	Ser	Lys	Asn	Ile	
			85						90					95		
ctt	gat	aca	gtt	gac	ttc	tcg	cag	agt	caa	ctt	ggg	cat	agt	aat	ttt	336
Leu	Asp	Thr	Val	Asp	Phe	Ser	Gln	Ser	Gln	Leu	Gly	His	Ser	Asn	Phe	
			100					105					110			
cgc	gaa	tgt	cag	att	aga	aat	tca	aac	ttc	gat	aat	tgt	tat	ctt	tac	384
Arg	Glu	Cys	Gln	Ile	Arg	Asn	Ser	Asn	Phe	Asp	Asn	Cys	Tyr	Leu	Tyr	
		115					120					125				
gct	tcg	cac	ttc	acc	aga	gca	gag	ttt	ctg	tct	gcc	aaa	gaa	ata	tca	432
Ala	Ser	His	Phe	Thr	Arg	Ala	Glu	Phe	Leu	Ser	Ala	Lys	Glu	Ile	Ser	
	130					135					140					
ttt	att	aaa	tcg	aat	ttg	aca	gct	gtt	atg	ttt	gat	tat	gtg	cga	atg	480
Phe	Ile	Lys	Ser	Asn	Leu	Thr	Ala	Val	Met	Phe	Asp	Tyr	Val	Arg	Met	
145					150					155					160	
tcg	aca	ggg	aat	ttt	aaa	gat	tgc	att	aca	gaa	caa	ttg	gaa	tta	act	528
Ser	Thr	Gly	Asn	Phe	Lys	Asp	Cys	Ile	Thr	Glu	Gln	Leu	Glu	Leu	Thr	
			165						170					175		
att	gat	tat	tca	gat	ata	ttt	tgg	aat	gaa	gat	ctc	gat	ggg	tat	atc	576
Ile	Asp	Tyr	Ser	Asp	Ile	Phe	Trp	Asn	Glu	Asp	Leu	Asp	Gly	Tyr	Ile	
			180					185						190		
aat	aac	att	ata	aaa	atg	att	gat	aca	ttg	cca	gat	aat	gca	atg	ata	624
Asn	Asn	Ile	Ile	Lys	Met	Ile	Asp	Thr	Leu	Pro	Asp	Asn	Ala	Met	Ile	
		195					200					205				
ttg	aaa	tcc	gtt	ctg	gcc	gta	aaa	ctg	gtg	atg	caa	tta	aaa	ata	ctt	672
Leu	Lys	Ser	Val	Leu	Ala	Val	Lys	Leu	Val	Met	Gln	Leu	Lys	Ile	Leu	

210

215

220

aat att gtt aat aaa aac ttt att gag aat atg aag aaa ata ttt agc 720
 Asn Ile Val Asn Lys Asn Phe Ile Glu Asn Met Lys Lys Ile Phe Ser
 225 230 235 240

cat tgt cct tat ata aaa gat ccc att ata cgc agt tat atc cat tct 768
 His Cys Pro Tyr Ile Lys Asp Pro Ile Ile Arg Ser Tyr Ile His Ser
 245 250 255

gat gaa gat aac aag ttc gat gat ttt atg cgt caa cat cga ttc agt 816
 Asp Glu Asp Asn Lys Phe Asp Asp Phe Met Arg Gln His Arg Phe Ser
 260 265 270

gag gtg aat ttc gat acc caa cag atg atc gat ttt att aac aga ttt 864
 Glu Val Asn Phe Asp Thr Gln Gln Met Ile Asp Phe Ile Asn Arg Phe
 275 280 285

aat acg aat aaa tgg cta att gat aaa aat aac aat ttt ttt atc caa 912
 Asn Thr Asn Lys Trp Leu Ile Asp Lys Asn Asn Asn Phe Phe Ile Gln
 290 295 300

ctt atc gat cag gcc tta cga tca acg gat gat atg atc aaa gca aat 960
 Leu Ile Asp Gln Ala Leu Arg Ser Thr Asp Asp Met Ile Lys Ala Asn
 305 310 315 320

gtt tgg cat ctt tat aaa gag tgg att cgt agt gat gat gtt tca cct 1008
 Val Trp His Leu Tyr Lys Glu Trp Ile Arg Ser Asp Asp Val Ser Pro
 325 330 335

ata ttt ata gaa act gaa gat aat tta aga acc ttt aac acg aat gaa 1056
 Ile Phe Ile Glu Thr Glu Asp Asn Leu Arg Thr Phe Asn Thr Asn Glu
 340 345 350

tta aca cga aac gat aat atc ttt atc ctg ttc tcc tca gtc gat gat 1104
 Leu Thr Arg Asn Asp Asn Ile Phe Ile Leu Phe Ser Ser Val Asp Asp
 355 360 365

ggg cca gtt atg gtg gta agc tcc cag cgc tta cat gat atg ttg aat 1152
 Gly Pro Val Met Val Val Ser Ser Gln Arg Leu His Asp Met Leu Asn
 370 375 380

cct aca aaa gat acc aat tgg aat tcc acg tat atc tac aaa tcc aga 1200
 Pro Thr Lys Asp Thr Asn Trp Asn Ser Thr Tyr Ile Tyr Lys Ser Arg
 385 390 395 400

cat gag atg ttg cct gtt aat ctt act cag gaa aca ctt ttc agc tcc 1248
 His Glu Met Leu Pro Val Asn Leu Thr Gln Glu Thr Leu Phe Ser Ser
 405 410 415

aaa tct cat ggt aaa tat gcg ctt ttc ccc att ttt act gcg agt tgg 1296
 Lys Ser His Gly Lys Tyr Ala Leu Phe Pro Ile Phe Thr Ala Ser Trp
 420 425 430

cga gct cat cgt ata atg aat aag ggt gtt taa 1329
 Arg Ala His Arg Ile Met Asn Lys Gly Val *
 435 440

<210> 205
 <211> 717
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(717)

<400> 205
 gtg gga cgt aaa tgg gcc aat att gtt gct aaa aaa acg gct aaa gac 48
 Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp
 1 5 10 15
 ggt gca acg tct aaa att tat gca aaa ttc ggt gta gaa atc tat gct 96
 Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala
 20 25 30
 gct gct aaa caa ggt gaa ccc gat cca gaa tta aac aca tct tta aaa 144
 Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys
 35 40 45
 ttc gtt att gaa cgt gca aag cag gca caa gtt cca aag cac gtt att 192
 Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile
 50 55 60
 gat aaa gca att gat aaa gcc aaa ggc ggc gga gat gaa acg ttc gtg 240
 Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val
 65 70 75 80
 cag gga cgt tat gaa ggc ttt ggt cct aat ggc tca atg att atc gcc 288
 Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala
 85 90 95
 gag aca ttg act tca aat gtt aac cgt acg att gct aac gtt cgc aca 336
 Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr
 100 105 110
 att ttc aat aaa aaa ggc ggc aat atc gga gcg gca ggt tct gtc agc 384
 Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser
 115 120 125
 tat atg ttt gac aat acg ggt gtg att gta ttt aaa ggg aca gac cct 432
 Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro
 130 135 140
 gac cat att ttt gaa att tta ctt gaa gct gaa gtt gat gtt cgt gat 480
 Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp
 145 150 155 160
 gtg act gaa gaa gaa ggt aac att gtt att tat act gaa cct act gac 528
 Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp
 165 170 175
 ctt cat aaa gga atc gcg gct cta aaa gca gct gga atc act gag ttc 576

Leu	His	Lys	Gly	Ile	Ala	Ala	Leu	Lys	Ala	Ala	Gly	Ile	Thr	Glu	Phe	
			180					185					190			
tca	aca	aca	gaa	tta	gaa	atg	att	gct	caa	tct	gaa	gtt	gag	ctt	tcc	624
Ser	Thr	Thr	Glu	Leu	Glu	Met	Ile	Ala	Gln	Ser	Glu	Val	Glu	Leu	Ser	
		195					200				205					
cca	gaa	gat	tta	gaa	atc	ttt	gaa	ggg	ctt	gtt	gat	gcc	ctt	gaa	gat	672
Pro	Glu	Asp	Leu	Glu	Ile	Phe	Glu	Gly	Leu	Val	Asp	Ala	Leu	Glu	Asp	
		210				215					220					
gac	gac	gat	gta	caa	aaa	gtt	tat	cat	aac	gtc	gca	aat	ctc	taa		717
Asp	Asp	Asp	Val	Gln	Lys	Val	Tyr	His	Asn	Val	Ala	Asn	Leu	*		
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<210> 206
 <211> 786
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(786)

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Met	Val	Leu	Met	Ser	Glu	Thr	Lys	Asn	Glu	Leu	Glu	Asp	Leu	Leu	Glu	
1				5				10					15			
aaa	gca	gca	act	gaa	ccg	gcg	cac	cgc	ccg	gcc	ttt	ttc	cgt	act	cta	96
Lys	Ala	Ala	Thr	Glu	Pro	Ala	His	Arg	Pro	Ala	Phe	Phe	Arg	Thr	Leu	
			20					25					30			
ctg	gaa	tcc	acc	gtc	tgg	gtg	cct	ggc	acg	gcg	gcg	cag	ggc	gag	gct	144
Leu	Glu	Ser	Thr	Val	Trp	Val	Pro	Gly	Thr	Ala	Ala	Gln	Gly	Glu	Ala	
		35					40					45				
gtg	gtt	gaa	gat	agc	gcg	ctt	gat	tta	cag	cac	tgg	gaa	aaa	gaa	gac	192
Val	Val	Glu	Asp	Ser	Ala	Leu	Asp	Leu	Gln	His	Trp	Glu	Lys	Glu	Asp	
	50					55					60					
ggc	acc	agc	gtc	att	cct	ttt	ttc	acc	tcg	tta	gaa	gca	ctt	caa	cag	240
Gly	Thr	Ser	Val	Ile	Pro	Phe	Phe	Thr	Ser	Leu	Glu	Ala	Leu	Gln	Gln	
	65				70					75					80	
gcg	gtt	gaa	gac	gaa	cag	gca	ttt	gtc	gta	atg	ccc	gtt	cgc	acg	ctg	288
Ala	Val	Glu	Asp	Glu	Gln	Ala	Phe	Val	Val	Met	Pro	Val	Arg	Thr	Leu	
				85				90						95		
ttt	gag	atg	aca	ctt	ggc	gaa	acg	ctc	ttc	ctt	aat	gcc	aaa	ctg	cca	336
Phe	Glu	Met	Thr	Leu	Gly	Glu	Thr	Leu	Phe	Leu	Asn	Ala	Lys	Leu	Pro	
			100					105					110			
acc	ggt	aaa	gaa	ttt	atg	ccg	cgt	gaa	atc	agt	ttg	ttg	att	ggt	gaa	384
Thr	Gly	Lys	Glu	Phe	Met	Pro	Arg	Glu	Ile	Ser	Leu	Leu	Ile	Gly	Glu	

ccg atg cag gaa tat ttc cat ttg acc aat ggt caa att ggt aat gct	144
Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala	
35 40 45	
atg tcg gta aac tca ttt gtc acc aca gtg ggc ttt ttt ctg tct att	192
Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile	
50 55 60	
tat ttt gcc gat aaa cta ccg cgc aga tac acc atg tca ttc tca ctc	240
Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu	
65 70 75 80	
att gcg aca gga tta ctg ggt gtt tat ttg acg aca atg ccg ggg tat	288
Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr	
85 90 95	
tgg ggc atc ctc ttt gtc tgg gcg cta ttt ggc gtt act tgc gac atg	336
Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met	
100 105 110	
atg aac tgg ccg gtc ttg ctc aag tcg gta agt cga ttg ggc aat agc	384
Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser	
115 120 125	
gaa caa caa ggt cgg ttg ttt ggc ttc ttc gaa aca ggg cgt ggc att	432
Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile	
130 135 140	
gtc gat acc gtg gtg gca ttt tct gcg ttg gca gta ttt acc tgg ttt	480
Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe	
145 150 155 160	
ggc agt ggc tta tta ggt ttt aaa gca ggc atc tgg ttc tat tcc ctt	528
Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu	
165 170 175	
att gtg att gcc gta ggc att att att ttc ttt gtc ctg aat gac aaa	576
Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys	
180 185 190	
gaa gag gca ccg tcc gtt gag gtg aaa aaa gaa gac gga gca tcg aaa	624
Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys	
195 200 205	
aac acc agt atg acc tcg gtg ctg aaa gac aaa act atc tgg ctt atc	672
Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile	
210 215 220	
gct ttt aac gtc ttc ttc gtt tac gcg gtt tac tgt ggc ctg aca ttc	720
Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe	
225 230 235 240	
ttc att cca ttc ctg aaa aac atc tat cta ttg ccc gtt gcg ctg gtg	768
Phe Ile Pro Phe Leu Lys Asn Ile Tyr Leu Leu Pro Val Ala Leu Val	
245 250 255	
ggg gct tac ggc atc att aac caa tac tgt ctg aaa atg att ggt gga	816

gcg ccc ttt ctc ctt ttt ctt gca gcg tgg gga gca gat aaa ctc tgg	96
Ala Pro Phe Leu Leu Phe Leu Ala Ala Trp Gly Ala Asp Lys Leu Trp	
20 25 30	
cct cta ccg ctg cat gaa gtc aat ccc gca cga gtg gtc gtg gcg cag	144
Pro Leu Pro Leu His Glu Val Asn Pro Ala Arg Val Val Val Ala Gln	
35 40 45	
gat ggt acg ccg ctc tgg cgc ttc gcc gat gct gac ggc atc tgg cgt	192
Asp Gly Thr Pro Leu Trp Arg Phe Ala Asp Ala Asp Gly Ile Trp Arg	
50 55 60	
tat ccg gta aca atc gaa gat gtt tct cca cgt tac ctt gaa gcg ctg	240
Tyr Pro Val Thr Ile Glu Asp Val Ser Pro Arg Tyr Leu Glu Ala Leu	
65 70 75 80	
atc aat tat gaa gat cgc tgg ttc tgg aag cat ccg ggg gtg aat cca	288
Ile Asn Tyr Glu Asp Arg Trp Phe Trp Lys His Pro Gly Val Asn Pro	
85 90 95	
ttc tcg gtg gcg cgc gca gca tgg caa gat ctc act tcg gga cgg gtt	336
Phe Ser Val Ala Arg Ala Ala Trp Gln Asp Leu Thr Ser Gly Arg Val	
100 105 110	
att tcc ggt ggc agc acg ctc act atg cag gtt gct cgt ctg ctt gat	384
Ile Ser Gly Gly Ser Thr Leu Thr Met Gln Val Ala Arg Leu Leu Asp	
115 120 125	
cct cac ccc aaa aca ttt ggc ggc aaa att cgc cag ctc tgg cgc gcg	432
Pro His Pro Lys Thr Phe Gly Gly Lys Ile Arg Gln Leu Trp Arg Ala	
130 135 140	
ttg caa ctg gaa tgg cat ctg tct aag cgt gaa att ctg acc ttg tat	480
Leu Gln Leu Glu Trp His Leu Ser Lys Arg Glu Ile Leu Thr Leu Tyr	
145 150 155 160	
ctt aac cgc gct ccg ttt ggc ggt acg ttg cag ggg atc ggt gcg gca	528
Leu Asn Arg Ala Pro Phe Gly Gly Thr Leu Gln Gly Ile Gly Ala Ala	
165 170 175	
agt tgg gct tat ctc gga aaa tcg cct gcg aat tta agc tat tcc gag	576
Ser Trp Ala Tyr Leu Gly Lys Ser Pro Ala Asn Leu Ser Tyr Ser Glu	
180 185 190	
gcg gca atg ctg gcg gtt ttg ccg caa gcg ccc agc cgt ctt cgc ccg	624
Ala Ala Met Leu Ala Val Leu Pro Gln Ala Pro Ser Arg Leu Arg Pro	
195 200 205	
gat cgt tgg ccg gag cgt gcc gaa gcc gcg cgt aat aaa gtg ctc gaa	672
Asp Arg Trp Pro Glu Arg Ala Glu Ala Ala Arg Asn Lys Val Leu Glu	
210 215 220	
cgg atg gcc gtg caa ggt gtg tgg tcc cgt gag cag gta aaa gag tca	720
Arg Met Ala Val Gln Gly Val Trp Ser Arg Glu Gln Val Lys Glu Ser	
225 230 235 240	

690	695	700	
cgt tta ccg ggc gca gcg gaa gcg act ttg ccg ttg caa tca agt gga			2160
Arg Leu Pro Gly Ala Ala Glu Ala Thr Leu Pro Leu Gln Ser Ser Gly			
705	710	715	720
ggg gca ggt gaa cgc tgg tgg ttt ctg aat ggc gaa ccg tta act gaa			2208
Gly Ala Gly Glu Arg Trp Trp Phe Leu Asn Gly Glu Pro Leu Thr Glu			
	725	730	735
cgc ggg cgc aac gtg acc ctg cat ttg acg gat aaa ggt gat tat caa			2256
Arg Gly Arg Asn Val Thr Leu His Leu Thr Asp Lys Gly Asp Tyr Gln			
	740	745	750
ttg ctg gtg atg gat gac gtg ggg caa atc gcg aca gtg aaa ttt gtc			2304
Leu Leu Val Met Asp Asp Val Gly Gln Ile Ala Thr Val Lys Phe Val			
	755	760	765
atg caa tag			2313
Met Gln *			
770			

<210> 209
 <211> 4962
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(4962)

<400> 209	
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Met Lys Lys Leu Arg Val Ala Ala Cys Met Leu Met Leu Ala Leu Ala	
1	5 10 15
ggg tgc gac aac aac gat aac gcg cca aca gcg gtg aaa aaa gat gcg	96
Gly Cys Asp Asn Asn Asp Asn Ala Pro Thr Ala Val Lys Lys Asp Ala	
	20 25 30
cct tct gaa gtt act aaa gcg gcc tct tca gaa aac gcg agt tca gca	144
Pro Ser Glu Val Thr Lys Ala Ala Ser Ser Glu Asn Ala Ser Ser Ala	
	35 40 45
aaa ctc tcc gtg ccg gag aga caa aaa ctg gcc caa cag agt gcc ggt	192
Lys Leu Ser Val Pro Glu Arg Gln Lys Leu Ala Gln Gln Ser Ala Gly	
	50 55 60
aag gtg ctg aca ttg ctg gat ctc tct gaa gtc caa ctt gat ggt gca	240
Lys Val Leu Thr Leu Leu Asp Leu Ser Glu Val Gln Leu Asp Gly Ala	
	65 70 75 80
gcc acg ctg gtg ctg acg ttc tcc atc cct ctc gac ccg gat cag gat	288
Ala Thr Leu Val Leu Thr Phe Ser Ile Pro Leu Asp Pro Asp Gln Asp	
	85 90 95

ttc	tca	cgc	gtt	att	cat	gtc	gtc	gat	aaa	aaa	agc	ggc	aaa	gtg	gat	336
Phe	Ser	Arg	Val	Ile	His	Val	Val	Asp	Lys	Lys	Ser	Gly	Lys	Val	Asp	
			100					105					110			
ggt	gcc	tgg	gag	ctg	tca	gat	aat	ctt	aaa	gag	tta	cgt	tta	cgc	cac	384
Gly	Ala	Trp	Glu	Leu	Ser	Asp	Asn	Leu	Lys	Glu	Leu	Arg	Leu	Arg	His	
		115					120					125				
ctc	gaa	ccg	aaa	cgt	gat	ttg	atc	gtt	act	att	ggc	aag	gag	gtc	aaa	432
Leu	Glu	Pro	Lys	Arg	Asp	Leu	Ile	Val	Thr	Ile	Gly	Lys	Glu	Val	Lys	
	130					135					140					
gca	ctc	aac	aac	gca	acc	ttc	agt	aaa	gat	tac	gaa	aaa	act	ata	act	480
Ala	Leu	Asn	Asn	Ala	Thr	Phe	Ser	Lys	Asp	Tyr	Glu	Lys	Thr	Ile	Thr	
145					150					155					160	
acc	cgc	gac	atc	caa	ccc	agc	gtc	ggg	ttt	gcc	agc	cgt	ggg	tgc	ctg	528
Thr	Arg	Asp	Ile	Gln	Pro	Ser	Val	Gly	Phe	Ala	Ser	Arg	Gly	Ser	Leu	
			165					170						175		
ctg	cct	ggc	aaa	gtc	gtt	gaa	ggg	ctg	ccg	gta	atg	gcg	ctc	aac	gtt	576
Leu	Pro	Gly	Lys	Val	Val	Glu	Gly	Leu	Pro	Val	Met	Ala	Leu	Asn	Val	
		180						185					190			
aat	aat	gtc	gat	gtt	aac	ttc	ttc	cgc	gtt	aag	cca	gaa	tct	ctg	cca	624
Asn	Asn	Val	Asp	Val	Asn	Phe	Phe	Arg	Val	Lys	Pro	Glu	Ser	Leu	Pro	
		195					200					205				
gca	ttc	att	agc	caa	tgg	gaa	tac	cgc	aat	tgc	ctg	gcg	aac	tgg	cag	672
Ala	Phe	Ile	Ser	Gln	Trp	Glu	Tyr	Arg	Asn	Ser	Leu	Ala	Asn	Trp	Gln	
	210					215					220					
tca	gac	aaa	ctg	ctg	cag	atg	gcg	gat	ctg	gtc	tac	acc	gga	cgg	ttt	720
Ser	Asp	Lys	Leu	Leu	Gln	Met	Ala	Asp	Leu	Val	Tyr	Thr	Gly	Arg	Phe	
225					230					235					240	
gat	ctc	aat	cct	gcg	cgt	aac	acc	cgt	gaa	aaa	tta	ttg	ctg	ccg	ctg	768
Asp	Leu	Asn	Pro	Ala	Arg	Asn	Thr	Arg	Glu	Lys	Leu	Leu	Leu	Pro	Leu	
			245					250						255		
ggc	gat	atc	aaa	ccg	ctt	cag	cag	gcg	ggc	gtg	tat	ctg	gct	gtg	atg	816
Gly	Asp	Ile	Lys	Pro	Leu	Gln	Gln	Ala	Gly	Val	Tyr	Leu	Ala	Val	Met	
		260						265					270			
aat	cag	gct	gga	cgt	tac	gat	tac	agt	aat	ccc	gcg	acg	ctg	ttt	acg	864
Asn	Gln	Ala	Gly	Arg	Tyr	Asp	Tyr	Ser	Asn	Pro	Ala	Thr	Leu	Phe	Thr	
		275					280					285				
tta	agt	gat	atc	ggc	gtt	tca	gct	cac	cgt	tat	cac	aat	cgt	ctg	gat	912
Leu	Ser	Asp	Ile	Gly	Val	Ser	Ala	His	Arg	Tyr	His	Asn	Arg	Leu	Asp	
	290					295					300					
atc	ttt	acc	caa	agt	ctg	gaa	aac	ggc	gcg							

545				550				555				560				
ttg	acg	ctg	gat	gat	aaa	ggg	cgc	ggc	gaa	gtt	tct	aca	gaa	agc	cag	1728
Leu	Thr	Leu	Asp	Asp	Lys	Gly	Arg	Gly	Glu	Val	Ser	Thr	Glu	Ser	Gln	
				565					570					575		
tg	aag	gaa	acg	cat	tcc	cca	tta	cag	gtt	att	ttc	cag	ggt	agt	ttg	1776
Trp	Lys	Glu	Thr	His	Ser	Pro	Leu	Gln	Val	Ile	Phe	Gln	Gly	Ser	Leu	
				580					585					590		
ctg	gaa	tcg	ggc	ggt	cgc	ccg	gtg	acg	cgc	cgc	gct	gag	cag	gct	atc	1824
Leu	Glu	Ser	Gly	Gly	Arg	Pro	Val	Thr	Arg	Arg	Ala	Glu	Gln	Ala	Ile	
				595					600					605		
tg	cct	gcc	gat	gca	ttg	ccg	ggg	atc	cgt	ccg	cag	ttc	gcc	tcg	aaa	1872
Trp	Pro	Ala	Asp	Ala	Leu	Pro	Gly	Ile	Arg	Pro	Gln	Phe	Ala	Ser	Lys	
				610					615					620		
tcg	gtt	tac	gat	tat	cgt	act	gac	agc	acg	gtg	aaa	cag	ccc	att	gtt	1920
Ser	Val	Tyr	Asp	Tyr	Arg	Thr	Asp	Ser	Thr	Val	Lys	Gln	Pro	Ile	Val	
				625					630					635		
gat	gaa	ggc	agt	aac	gcc	gct	ttt	gac	atc	gtt	tat	agc	gat	gcg	caa	1968
Asp	Glu	Gly	Ser	Asn	Ala	Ala	Phe	Asp	Ile	Val	Tyr	Ser	Asp	Ala	Gln	
				645					650					655		
ggc	gtg	aaa	aaa	gcc	gtg	tcg	ggc	ttg	cag	gtg	cgc	ctg	att	cgc	gaa	2016
Gly	Val	Lys	Lys	Ala	Val	Ser	Gly	Leu	Gln	Val	Arg	Leu	Ile	Arg	Glu	
				660					665					670		
cgc	cgc	gat	tac	tac	tgg	aac	tgg	tca	gaa	gat	gaa	ggc	tgg	cag	tca	2064
Arg	Arg	Asp	Tyr	Tyr	Trp	Asn	Trp	Ser	Glu	Asp	Glu	Gly	Trp	Gln	Ser	
				675					680					685		
cag	ttt	gat	caa	aaa	gat	ctg	atc	gaa	aat	gaa	caa	act	ctg	gat	ctg	2112
Gln	Phe	Asp	Gln	Lys	Asp	Leu	Ile	Glu	Asn	Glu	Gln	Thr	Leu	Asp	Leu	
				690					695					700		
aaa	gcg	gac	gaa	acc	ggc	aag	gtc	agt	ttt	ccg	gta	gag	tgg	ggc	gct	2160
Lys	Ala	Asp	Glu	Thr	Gly	Lys	Val	Ser	Phe	Pro	Val	Glu	Trp	Gly	Ala	
				705					710					715		
tat	cgt	ctg	gaa	gtc	aaa	gcg	ccg	aat	gaa	gcg	gtc	agt	agt	gtt	cgt	2208
Tyr	Arg	Leu	Glu	Val	Lys	Ala	Pro	Asn	Glu	Ala	Val	Ser	Ser	Val	Arg	
				725					730					735		
ttc	tgg	gct	ggc	tat	agc	tgg	cag	gac	aac	agc	gac	ggt	agc	ggc	gca	2256
Phe	Trp	Ala	Gly	Tyr	Ser	Trp	Gln	Asp	Asn	Ser	Asp	Gly	Ser	Gly	Ala	
				740					745					750		
gtg	cga	ccc	gac	cgt	gtc	acg	ctg	aaa	ctg	gat	aaa	gcc	agt	tat	cgc	2304
Val	Arg	Pro	Asp	Arg	Val	Thr	Leu	Lys	Leu	Asp	Lys	Ala	Ser	Tyr	Arg	
				755					760					765		
cct	ggc	gac	acc	att	aag	ttg	cat	atc	gcc	gcg	cca	acg	gcg	ggt	aaa	2352
Pro	Gly	Asp	Thr	Ile	Lys	Leu	His	Ile	Ala	Ala	Pro	Thr	Ala	Gly	Lys	
				770					775					780		

ggt tat gcg atg gtc gag tcc agt gaa ggg ccg ctg tgg tgg caa gag	2400
Gly Tyr Ala Met Val Glu Ser Ser Glu Gly Pro Leu Trp Trp Gln Glu	
785 790 795 800	
att gat gtt cgg gct caa ggg ctg gat ctg acg att ccg gtc gat aaa	2448
Ile Asp Val Arg Ala Gln Gly Leu Asp Leu Thr Ile Pro Val Asp Lys	
805 810 815	
acc tgg aat cgt cat gat ctg tat tta agt acg ctg gtg gta cgt cct	2496
Thr Trp Asn Arg His Asp Leu Tyr Leu Ser Thr Leu Val Val Arg Pro	
820 825 830	
ggc gat aaa tct cgc tcc gcg acg cca aaa cgc gcg gtt ggt gtg ttg	2544
Gly Asp Lys Ser Arg Ser Ala Thr Pro Lys Arg Ala Val Gly Val Leu	
835 840 845	
cat ctg ccg ctt ggc gat gaa aac cgt cgc ctc gat ctg gcg ctg gaa	2592
His Leu Pro Leu Gly Asp Glu Asn Arg Arg Leu Asp Leu Ala Leu Glu	
850 855 860	
aca cca gca aaa atg cgt ccc aat caa cca tta acc gtg aaa att aaa	2640
Thr Pro Ala Lys Met Arg Pro Asn Gln Pro Leu Thr Val Lys Ile Lys	
865 870 875 880	
gcc agc act aaa aat ggc gag aag cct aaa cag gtg aat gtg ctg gtg	2688
Ala Ser Thr Lys Asn Gly Glu Lys Pro Lys Gln Val Asn Val Leu Val	
885 890 895	
tct gcc gtt gat agt ggt gtg ctg aat att act gac tac gtc acg cca	2736
Ser Ala Val Asp Ser Gly Val Leu Asn Ile Thr Asp Tyr Val Thr Pro	
900 905 910	
gat ccg tgg cag gcg ttc ttt ggt cag aaa cgc tat ggc gca gac att	2784
Asp Pro Trp Gln Ala Phe Phe Gly Gln Lys Arg Tyr Gly Ala Asp Ile	
915 920 925	
tac gat att tac ggt cag gtt att gaa ggt cag ggg cgt ctg gca gct	2832
Tyr Asp Ile Tyr Gly Gln Val Ile Glu Gly Gln Gly Arg Leu Ala Ala	
930 935 940	
ctg cgt ttc ggt ggc gat ggt gat gag ctg aaa cgt ggt ggt aaa ccg	2880
Leu Arg Phe Gly Gly Asp Gly Asp Glu Leu Lys Arg Gly Gly Lys Pro	
945 950 955 960	
ccg gtc aat cac gtc aat att gtc gtg cag cag gcg ctg ccg gta acg	2928
Pro Val Asn His Val Asn Ile Val Val Gln Gln Ala Leu Pro Val Thr	
965 970 975	
ctc aac gaa cag ggc gaa ggc tcg gtt aca ctg ccg att ggc gat ttt	2976
Leu Asn Glu Gln Gly Glu Gly Ser Val Thr Leu Pro Ile Gly Asp Phe	
980 985 990	
aac ggt gaa ttg cgc gtc atg gcg caa gcc tgg acg gca gat gac ttc	3024
Asn Gly Glu Leu Arg Val Met Ala Gln Ala Trp Thr Ala Asp Asp Phe	
995 1000 1005	

<221> CDS
 <222> (1)...(795)

<400> 210

atg gat ctg ttg tac cgg gta aaa acg ctt tgg gcc gcg ctg cgc ggt	48
Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly	
1 5 10 15	
aat cat tac acc tgg cct gcc atc gat atc acc ctc ccc ggc aat cgc	96
Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg	
20 25 30	
cat ttt cat ctg att ggc agt att cat atg ggt agc cac gat atg gct	144
His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala	
35 40 45	
ccc ctg ccc acc cgt ttg ctc aaa aag ctc aaa aac gcc gat gcg ctg	192
Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu	
50 55 60	
atc gtc gag gcg gat gtt tcc acc agc gat acg cct ttt gct aat ttg	240
Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu	
65 70 75 80	
cct gcc tgc gag gcg ctg gaa gag cgc att agc gag gag caa ctc caa	288
Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln	
85 90 95	
aac ctg cag cac att agc cag gag atg ggc att tct ccc tca ctc ttt	336
Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe	
100 105 110	
tct acc caa ccg ctg tgg caa atc gcg atg gtt ctt cag gcg acg cag	384
Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln	
115 120 125	
gca caa aaa ctg ggg ctg cgg gca gaa tac ggt atc gat tac cag cta	432
Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu	
130 135 140	
ttg cag gcg gcg aag caa caa cat aaa ccc gtg att gaa ctg gaa ggg	480
Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly	
145 150 155 160	
gct gaa aac cag att gcc atg ttg ctc cag ctc cct gac aaa gga ctg	528
Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu	
165 170 175	
gcg ctg ctg gac gat acg ctg acc cac tgg cat acc aac gca cgg ttg	576
Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu	
180 185 190	
ctg caa caa atg atg agc tgg tgg ctg aat gca ccg ccg caa aat aat	624
Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn	
195 200 205	
gat ata acg ctg ccc aat acg ttc agt cag tcg ctg tac gat gtg ctg	672

Asp	Ile	Thr	Leu	Pro	Asn	Thr	Phe	Ser	Gln	Ser	Leu	Tyr	Asp	Val	Leu	
210						215					220					
atg	cat	cag	cga	aat	ctc	gcc	tgg	cgg	gat	aaa	tta	cgc	gcc	atg	ccg	720
Met	His	Gln	Arg	Asn	Leu	Ala	Trp	Arg	Asp	Lys	Leu	Arg	Ala	Met	Pro	
225					230					235					240	
ccg	ggg	cga	tat	gtg	gtc	gcg	gtc	ggg	gca	cta	cac	ctg	tat	gga	gaa	768
Pro	Gly	Arg	Tyr	Val	Val	Ala	Val	Gly	Ala	Leu	His	Leu	Tyr	Gly	Glu	
				245					250					255		
ggg	aat	ttg	ccg	caa	atg	ttg	cgc	taa								795
Gly	Asn	Leu	Pro	Gln	Met	Leu	Arg	*								
				260												

<210> 211
 <211> 969
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(969)

<400> 211																
atg	gat	aat	ttt	ctt	gct	ctg	acc	tta	acg	ggg	aaa	aaa	ccg	gtt	atc	48
Met	Asp	Asn	Phe	Leu	Ala	Leu	Thr	Leu	Thr	Gly	Lys	Lys	Pro	Val	Ile	
1				5					10					15		
acc	gag	cga	gaa	atc	aac	ggc	gtt	cgc	tgg	cgc	tgg	ctg	ggc	gat	ggg	96
Thr	Glu	Arg	Glu	Ile	Asn	Gly	Val	Arg	Trp	Arg	Trp	Leu	Gly	Asp	Gly	
			20					25					30			
gtg	ctg	gaa	ctg	acg	cca	tta	acg	cca	ccg	caa	ggc	gca	ctg	gtg	att	144
Val	Leu	Glu	Leu	Thr	Pro	Leu	Thr	Pro	Pro	Gln	Gly	Ala	Leu	Val	Ile	
			35				40					45				
tca	gcg	gga	ata	cac	ggg	aat	gag	acg	gca	cct	gtg	gag	atg	ctg	gac	192
Ser	Ala	Gly	Ile	His	Gly	Asn	Glu	Thr	Ala	Pro	Val	Glu	Met	Leu	Asp	
	50					55				60						
gcg	ttg	ctt	ggc	gcg	ata	tct	cac	ggc	gag	atc	ccg	tta	cgt	tgg	cgg	240
Ala	Leu	Leu	Gly	Ala	Ile	Ser	His	Gly	Glu	Ile	Pro	Leu	Arg	Trp	Arg	
65					70					75					80	
ttg	ctg	gtg	atc	ctc	ggg	aat	cct	cct	gcg	ctg	aag	caa	ggg	aaa	cgt	288
Leu	Leu	Val	Ile	Leu	Gly	Asn	Pro	Pro	Ala	Leu	Lys	Gln	Gly	Lys	Arg	
				85					90					95		
tat	tgc	cat	agc	gat	atg	aat	cga	atg	ttt	ggc	ggg	cgt	tgg	cag	cta	336
Tyr	Cys	His	Ser	Asp	Met	Asn	Arg	Met	Phe	Gly	Gly	Arg	Trp	Gln	Leu	
			100					105					110			
ttt	gct	gaa	agc	gga	gaa	acc	tgt	cgg	gcg	cgc	gaa	ctg	gaa	cag	tgc	384
Phe	Ala	Glu	Ser	Gly	Glu	Thr	Cys	Arg	Ala	Arg	Glu	Leu	Glu	Gln	Cys	
		115					120					125				

ctg gaa gat ttt tat gac cag ggc aaa gaa tct gtg cgc tgg cac ctt	432
Leu Glu Asp Phe Tyr Asp Gln Gly Lys Glu Ser Val Arg Trp His Leu	
130 135 140	
gat cta cat acc gca att cgt ggc tcc ttg cat ccg cag ttc ggt gta	480
Asp Leu His Thr Ala Ile Arg Gly Ser Leu His Pro Gln Phe Gly Val	
145 150 155 160	
tta ccg caa cgc gac att ccc tgg gac gag aaa ttt ctg acg tgg ctg	528
Leu Pro Gln Arg Asp Ile Pro Trp Asp Glu Lys Phe Leu Thr Trp Leu	
165 170 175	
ggt gcg gcg ggg ctg gag gcg ctg gtg ttc cat cag gaa cct ggt ggt	576
Gly Ala Ala Gly Leu Glu Ala Leu Val Phe His Gln Glu Pro Gly Gly	
180 185 190	
acg ttt acc cat ttc agc gcc aga cat ttt ggc gcg ctg gcc tgt acg	624
Thr Phe Thr His Phe Ser Ala Arg His Phe Gly Ala Leu Ala Cys Thr	
195 200 205	
ctg gaa ctt ggc aaa gcg ttg ccc ttt ggg caa aac gat ctt cgc cag	672
Leu Glu Leu Gly Lys Ala Leu Pro Phe Gly Gln Asn Asp Leu Arg Gln	
210 215 220	
ttt gca gta act gcc agc gca att gct gcg ctg cta tct ggt gag agt	720
Phe Ala Val Thr Ala Ser Ala Ile Ala Ala Leu Leu Ser Gly Glu Ser	
225 230 235 240	
gtc ggt atc gtg aga aca ccg ccg ctc cgt tat ccg gtg gtt tcg caa	768
Val Gly Ile Val Arg Thr Pro Pro Leu Arg Tyr Arg Val Val Ser Gln	
245 250 255	
att act cgc cac tcg ccg tcc ttc gaa atg cat atg gca agt gac acg	816
Ile Thr Arg His Ser Pro Ser Phe Glu Met His Met Ala Ser Asp Thr	
260 265 270	
ctg aat ttt atg ccg ttt gag aaa gga aca ttg ctg gcg cag gac gga	864
Leu Asn Phe Met Pro Phe Glu Lys Gly Thr Leu Leu Ala Gln Asp Gly	
275 280 285	
gag gaa cgt ttt acc gta acc cat gat gta gag tat gtg tta ttc cct	912
Glu Glu Arg Phe Thr Val Thr His Asp Val Glu Tyr Val Leu Phe Pro	
290 295 300	
aat ccg ttg gta gcg ttg gga tta cgc gcg gga tta atg ctc gaa aaa	960
Asn Pro Leu Val Ala Leu Gly Leu Arg Ala Gly Leu Met Leu Glu Lys	
305 310 315 320	
ata agc taa	969
Ile Ser *	

<210> 212
 <211> 1344
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1344)

<400> 212

atg aac gcc tgg gaa gtc aat ttc gac ggg ctg gta ggg ctg acg cat	48
Met Asn Ala Trp Glu Val Asn Phe Asp Gly Leu Val Gly Leu Thr His	
1 5 10 15	
cat tac gcg ggc ctg tcg ttt ggt aat gaa gcc tct acc cgt cac cgt	96
His Tyr Ala Gly Leu Ser Phe Gly Asn Glu Ala Ser Thr Arg His Arg	
20 25 30	
ttt cag gtg tct aac ccg cga ctg gcg gcg aag cag ggc tta ctg aaa	144
Phe Gln Val Ser Asn Pro Arg Leu Ala Ala Lys Gln Gly Leu Leu Lys	
35 40 45	
atg aaa gcc ctt gcc gat gcg gga ttc ccc cag gcc gtg atc ccg ccg	192
Met Lys Ala Leu Ala Asp Ala Gly Phe Pro Gln Ala Val Ile Pro Pro	
50 55 60	
cac gag cgt ccg ttt att ccg gtg ctg cgt cag ttg gga ttc agt ggt	240
His Glu Arg Pro Phe Ile Pro Val Leu Arg Gln Leu Gly Phe Ser Gly	
65 70 75 80	
agc gat gag cag gta ctg gaa aaa gtt gca cgc cag gca ccg cac tgg	288
Ser Asp Glu Gln Val Leu Glu Lys Val Ala Arg Gln Ala Pro His Trp	
85 90 95	
ctt tcc agc gtc agt tcc gct tcg cca atg tgg gta gcc aat gcg gca	336
Leu Ser Ser Val Ser Ser Ala Ser Pro Met Trp Val Ala Asn Ala Ala	
100 105 110	
acg atc gcg cca tct gcc gat acg ctg gat ggc aaa gtg cat ctc acc	384
Thr Ile Ala Pro Ser Ala Asp Thr Leu Asp Gly Lys Val His Leu Thr	
115 120 125	
gtt gcc aac ctg aac aat aaa ttt cac cgt tcg ctg gaa gcg ccc gtc	432
Val Ala Asn Leu Asn Asn Lys Phe His Arg Ser Leu Glu Ala Pro Val	
130 135 140	
act gaa tcg ctg tta aaa gcg att ttt aac gac gaa gag aaa ttt agc	480
Thr Glu Ser Leu Leu Lys Ala Ile Phe Asn Asp Glu Glu Lys Phe Ser	
145 150 155 160	
gtc cat tcg gcg ttg cca cag gta gcg ttg ctc ggt gat gag ggg gcg	528
Val His Ser Ala Leu Pro Gln Val Ala Leu Leu Gly Asp Glu Gly Ala	
165 170 175	
gca aac cac aat cgt ctc ggc ggt cat tac ggt gaa ccg ggt atg caa	576
Ala Asn His Asn Arg Leu Gly Gly His Tyr Gly Glu Pro Gly Met Gln	
180 185 190	
ctt ttt gtc tac ggg cga gaa gaa ggc aat gat acc cgg cct tcc cgt	624
Leu Phe Val Tyr Gly Arg Glu Glu Gly Asn Asp Thr Arg Pro Ser Arg	

205

672

720

768

816

864

912

960

100

105

110

11.

12

12

12

ctc ggt tgc gtt tat ccg ttc cag cgc gag gga ggg ggc aat gga taa 1344
 Leu Gly Ser Val Tyr Pro Phe Gln Arg Glu Gly Gly Gly Asn Gly *
 435 440 445

<210> 213
 <211> 1479
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1479)

<400> 213
 atg act tta tgg att aac ggt gac tgg ata acg ggc cag ggc gca tgc 48
 Met Thr Leu Trp Ile Asn Gly Asp Trp Ile Thr Gly Gln Gly Ala Ser
 1 5 10 15

cgt gtg aag cgt aat ccg gta tgc ggc gag gtg tta tgg caa ggc aat 96
 Arg Val Lys Arg Asn Pro Val Ser Gly Glu Val Leu Trp Gln Gly Asn
 20 25 30

gat gcc gat gcc gct cag gtc gag cag gct tgt cgg gca gcc cgt gcg 144
 Asp Ala Asp Ala Ala Gln Val Glu Gln Ala Cys Arg Ala Ala Arg Ala
 35 40 45

gcg ttt ccg cgc tgg gcg cgg ctt tca ttt gct gaa cgt cat gcc gtt 192
 Ala Phe Pro Arg Trp Ala Arg Leu Ser Phe Ala Glu Arg His Ala Val
 50 55 60

gtc gaa cgc ttt gcc gca ctg ctg gaa agc aat aaa gcc gaa tta acc 240
 Val Glu Arg Phe Ala Ala Leu Leu Glu Ser Asn Lys Ala Glu Leu Thr
 65 70 75 80

gcg att att gcc aga gaa acg ggt aag ccg cgc tgg gaa gcg gca acc 288
 Ala Ile Ile Ala Arg Glu Thr Gly Lys Pro Arg Trp Glu Ala Ala Thr
 85 90 95

gaa gtg acg gcg atg atc aat aaa atc gcg ata tca att aag gcg tat 336
 Glu Val Thr Ala Met Ile Asn Lys Ile Ala Ile Ser Ile Lys Ala Tyr
 100 105 110

cac gtt cgt acc ggc gag cag cgt agt gaa atg ccg gac ggc gcg gcg 384
 His Val Arg Thr Gly Glu Gln Arg Ser Glu Met Pro Asp Gly Ala Ala
 115 120 125

agc ctg cga cat cgc ccg cac ggc gtg ctg gcg gtg ttt ggg ccg tat 432
 Ser Leu Arg His Arg Pro His Gly Val Leu Ala Val Phe Gly Pro Tyr
 130 135 140

aat ttc cct ggt cat ttg ccg aac gga cat atc gtt ccg gca ttg ctg 480
 Asn Phe Pro Gly His Leu Pro Asn Gly His Ile Val Pro Ala Leu Leu
 145 150 155 160

Arg	Tyr	Asp	Thr	Phe	Asp	Glu	Ala	Ile	Arg	Met	Ala	Asn	Asn	Thr	Arg	
385					390					395					400	
ttc	gga	ctc	tct	tgc	ggt	ctg	ggt	tcc	ccc	gag	cgg	gaa	aag	ttc	gat	1248
Phe	Gly	Leu	Ser	Cys	Gly	Leu	Val	Ser	Pro	Glu	Arg	Glu	Lys	Phe	Asp	
				405					410					415		
caa	ctg	ttg	ctg	gag	gcg	cgg	gcg	ggg	att	ggt	aac	tgg	aac	aaa	ccg	1296
Gln	Leu	Leu	Leu	Glu	Ala	Arg	Ala	Gly	Ile	Val	Asn	Trp	Asn	Lys	Pro	
			420					425					430			
ctt	acc	ggt	gct	gcc	agt	acc	gcg	cca	ttc	ggc	ggc	att	ggt	gct	tcc	1344
Leu	Thr	Gly	Ala	Ala	Ser	Thr	Ala	Pro	Phe	Gly	Gly	Ile	Gly	Ala	Ser	
		435					440					445				
ggt	aac	cat	cgc	ccc	agc	gcc	tgg	tat	gcc	gca	gat	tac	tgc	gca	tgg	1392
Gly	Asn	His	Arg	Pro	Ser	Ala	Trp	Tyr	Ala	Ala	Asp	Tyr	Cys	Ala	Trp	
	450					455					460					
ccg	atg	gcg	agc	ctg	gag	tcg	gac	tcg	tta	aca	ttg	ccc	gcc	acg	ctt	1440
Pro	Met	Ala	Ser	Leu	Glu	Ser	Asp	Ser	Leu	Thr	Leu	Pro	Ala	Thr	Leu	
	465				470					475					480	
aac	ccc	ggg	ctg	gat	ttt	tcc	gat	gag	gtg	gtg	cga	tga				1479
Asn	Pro	Gly	Leu	Asp	Phe	Ser	Asp	Glu	Val	Val	Arg	*				
			485					490								
<210> 214																
<211> 1035																
<212> DNA																
<213> Escherichia coli																
<220>																
<221> CDS																
<222> (1)...(1035)																
<400> 214																
atg	atg	gtc	atc	cgt	ccc	ggt	gag	cga	tca	gat	gtc	tcg	gcg	ctg	atg	48
Met	Met	Val	Ile	Arg	Pro	Val	Glu	Arg	Ser	Asp	Val	Ser	Ala	Leu	Met	
1				5					10					15		
cag	ctt	gcc	agc	aaa	acg	ggc	ggc	ggc	ctg	acg	tcg	ctt	ccc	gcc	aat	96
Gln	Leu	Ala	Ser	Lys	Thr	Gly	Gly	Gly	Leu	Thr	Ser	Leu	Pro	Ala	Asn	
			20					25					30			
gaa	gcc	acg	ctt	tcg	gcg	cgt	atc	gaa	agg	gca	atc	aaa	acc	tgg	caa	144
Glu	Ala	Thr	Leu	Ser	Ala	Arg	Ile	Glu	Arg	Ala	Ile	Lys	Thr	Trp	Gln	
		35					40					45				
ggc	gaa	ctg	ccc	aaa	agt	gag	cag	ggc	tat	gtg	ttc	gtg	ctg	gaa	gat	192
Gly	Glu	Leu	Pro	Lys	Ser	Glu	Gln	Gly	Tyr	Val	Phe	Val	Leu	Glu	Asp	
		50				55					60					
agc	gag	aca	ggc	acc	gtg	gcg	ggg	att	tgt	gcc	att	gag	gtg	gcg	gtt	240
Ser	Glu	Thr	Gly	Thr	Val	Ala	Gly	Ile	Cys	Ala	Ile	Glu	Val	Ala	Val	
	65				70				75						80	

gtg cgt acc gat ccg gca acc gag cgt ttg att tta acc gcc gca caa 960
Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln
305 310 315 320

ctg gat gcc ctc aaa tgc cac gcc ggg gat cgc gtt cgt ctg gtg cgc 1008
Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg
325 330 335

ctg tgc gca gag gag aaa aca gca tga 1035
Leu Cys Ala Glu Glu Lys Thr Ala *

<210> 215
<211> 1221
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1221)

<400> 215
atg tct cag cca att acg cgt gaa aac ttt gat gaa tgg atg ata cct 48
Met Ser Gln Pro Ile Thr Arg Glu Asn Phe Asp Glu Trp Met Ile Pro
1 5 10 15

gtt tac gct ccg gca ccc ttt ata ccg gta cgt ggc gaa ggt tcg cgc 96
Val Tyr Ala Pro Ala Pro Phe Ile Pro Val Arg Gly Glu Gly Ser Arg
20 25 30

ttg tgg gat cag cag ggg aaa gag tat atc gac ttc gcg ggt ggc att 144
Leu Trp Asp Gln Gln Gly Lys Glu Tyr Ile Asp Phe Ala Gly Gly Ile
35 40 45

gcg gtg aac gcg ctg ggc cat gcg cat ccg gaa ctg cgt gaa gcg ctg 192
Ala Val Asn Ala Leu Gly His Ala His Pro Glu Leu Arg Glu Ala Leu
50 55 60

aac gaa cag gcg agt aag ttc tgg cat acc ggc aac ggt tac acc aac 240
Asn Glu Gln Ala Ser Lys Phe Trp His Thr Gly Asn Gly Tyr Thr Asn
65 70 75 80

gag ccg gta ctg cga ctg gcg aaa aaa ttg atc gac gcc acg ttt gcc 288
Glu Pro Val Leu Arg Leu Ala Lys Lys Leu Ile Asp Ala Thr Phe Ala
85 90 95

gat cgc gtc ttc ttt tgt aac tcc ggt gcg gaa gcc aac gaa gcg gcg 336
Asp Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
100 105 110

cta aaa ctg gcg cgt aaa ttc gct cac gac cgc tac ggc agc cat aag 384
Leu Lys Leu Ala Arg Lys Phe Ala His Asp Arg Tyr Gly Ser His Lys
115 120 125

agc ggc atc gtg gcg ttc aaa aat gcg ttt cat ggt cgc acg ctg ttt 432
Ser Gly Ile Val Ala Phe Lys Asn Ala Phe His Gly Arg Thr Leu Phe

130				135				140								
act	gtc	agt	gcg	ggg	ggg	cag	cca	gcc	tat	tca	cag	gat	ttt	gcg	cca	480
Thr	Val	Ser	Ala	Gly	Gly	Gln	Pro	Ala	Tyr	Ser	Gln	Asp	Phe	Ala	Pro	
145				150				155				160				
ctg	ccg	gcg	gat	att	cgt	cat	gct	gca	tat	aac	gat	att	aac	tct	gcc	528
Leu	Pro	Ala	Asp	Ile	Arg	His	Ala	Ala	Tyr	Asn	Asp	Ile	Asn	Ser	Ala	
165				170				175								
agc	gcg	ctg	att	gac	gac	tct	acc	tgt	gcg	gtg	att	gtc	gaa	ccc	atc	576
Ser	Ala	Leu	Ile	Asp	Asp	Ser	Thr	Cys	Ala	Val	Ile	Val	Glu	Pro	Ile	
180				185				190								
cag	ggg	gaa	ggc	ggg	gtg	gtg	cca	gcc	agc	aac	gcg	ttt	tta	caa	ggt	624
Gln	Gly	Glu	Gly	Gly	Val	Val	Pro	Ala	Ser	Asn	Ala	Phe	Leu	Gln	Gly	
195				200				205								
ctg	cgt	gaa	ttg	tgt	aac	cgc	cac	aat	gcg	ctg	ttg	att	ttt	gat	gaa	672
Leu	Arg	Glu	Leu	Cys	Asn	Arg	His	Asn	Ala	Leu	Leu	Ile	Phe	Asp	Glu	
210				215				220								
gta	caa	acc	ggc	gtc	ggg	cgc	acc	ggg	gaa	ctg	tat	gcc	tat	atg	cac	720
Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Glu	Leu	Tyr	Ala	Tyr	Met	His	
225				230				235								
tac	ggc	gtg	acg	cct	gat	ctg	tta	act	acc	gcc	aaa	gcg	ctg	ggc	ggc	768
Tyr	Gly	Val	Thr	Pro	Asp	Leu	Leu	Thr	Thr	Ala	Lys	Ala	Leu	Gly	Gly	
245				250				255								
ggt	ttc	ccg	gtc	ggg	gcg	ttg	ttg	gca	acc	gaa	gag	tgc	gcc	cgc	gtg	816
Gly	Phe	Pro	Val	Gly	Ala	Leu	Leu	Ala	Thr	Glu	Glu	Cys	Ala	Arg	Val	
260				265				270								
atg	acc	gtt	ggc	act	cat	ggc	acc	acc	tat	ggc	ggt	aat	ccg	ctg	gcc	864
Met	Thr	Val	Gly	Thr	His	Gly	Thr	Thr	Tyr	Gly	Gly	Asn	Pro	Leu	Ala	
275				280				285								
tcg	gcg	gtg	gca	ggc	aaa	gtg	ctg	gag	ctc	atc	aac	aca	cca	gag	atg	912
Ser	Ala	Val	Ala	Gly	Lys	Val	Leu	Glu	Leu	Ile	Asn	Thr	Pro	Glu	Met	
290				295				300								
ctt	aat	ggc	gtt	aaa	cag	cgt	cac	gac	tgg	ttt	gtt	gag	cgt	ctt	aat	960
Leu	Asn	Gly	Val	Lys	Gln	Arg	His	Asp	Trp	Phe	Val	Glu	Arg	Leu	Asn	
305				310				315								
act	att	aat	cac	cgc	tat	ggt	ttg	ttc	agt	gaa	gtt	cgc	ggc	tta	ggt	1008
Thr	Ile	Asn	His	Arg	Tyr	Gly	Leu	Phe	Ser	Glu	Val	Arg	Gly	Leu	Gly	
325				330				335								
ttg	ctg	att	ggc	tgt	gta	ctg	aat	gcc	gat	tac	gcc	ggg	caa	gcg	aaa	1056
Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Ala	Asp	Tyr	Ala	Gly	Gln	Ala	Lys	
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cag	atc	tct	cag	gaa	gcg	gcg	aaa	gca	ggc	gtg	atg	gta	ctg	att	gcg	1104
Gln	Ile	Ser	Gln	Glu	Ala	Ala	Lys	Ala	Gly	Val	Met	Val	Leu	Ile	Ala	
355				360				365								

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Gly Gly Asn Val Val Arg Phe Ala Pro Ala Leu Asn Val Ser Glu Glu	
370 375 380	
gag gtg acg acc gga ctg gat cgc ttt gca gct gct tgc gaa cac ttt	1200
Glu Val Thr Thr Gly Leu Asp Arg Phe Ala Ala Cys Glu His Phe	
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gaa tgg aag att gat ttc acc cgc gag ccg ttc gcc agc aac ggg ctg	96
Glu Trp Lys Ile Asp Phe Thr Arg Glu Pro Phe Ala Ser Asn Gly Leu	
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ttt gct att acc ggc cca aca ggt gcg ggg aaa acc acc ctg ctg gac	144
Phe Ala Ile Thr Gly Pro Thr Gly Ala Gly Lys Thr Thr Leu Leu Asp	
35 40 45	
gcc att tgt ctg gcg ctg tat cac gaa act ccg cgt ctc tct aac gtt	192
Ala Ile Cys Leu Ala Leu Tyr His Glu Thr Pro Arg Leu Ser Asn Val	
50 55 60	
tca caa tcg caa aat gat ctc atg acc cgc gat acc gcc gaa tgt ctg	240
Ser Gln Ser Gln Asn Asp Leu Met Thr Arg Asp Thr Ala Glu Cys Leu	
65 70 75 80	
gcg gag gtg gag ttt gaa gtg aaa ggt gaa gcg tac cgt gca ttc tgg	288
Ala Glu Val Glu Phe Glu Val Lys Gly Glu Ala Tyr Arg Ala Phe Trp	
85 90 95	
agc cag aat ccg gcg cgt aac caa ccc gac ggt aat ttg cag gtg cca	336
Ser Gln Asn Arg Ala Arg Asn Gln Pro Asp Gly Asn Leu Gln Val Pro	
100 105 110	
cgc gta gag ctg gcg cgc tgc gcc gac ggc aaa att ctc gcc gac aaa	384
Arg Val Glu Leu Ala Arg Cys Ala Asp Gly Lys Ile Leu Ala Asp Lys	
115 120 125	
gtg aaa gat aag ctg gaa ctg aca gcg acg tta acc ggg ctg gat tac	432

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	370					375				380						
tgg Trp	cag Gln	caa Gln	cag Gln	tta Leu	acc Thr	cat His	gct Ala	gag Glu	caa Gln	aaa Lys	ctt Leu	aat Asn	gcg Ala	ctt Leu	gcg Ala	1200
385					390					395					400	
gcg Ala	atc Ile	acg Thr	ttg Leu	acg Thr	tta Leu	acc Thr	gcc Ala	gat Asp	gaa Glu	gtt Val	gct Ala	acc Thr	gcc Ala	ctg Leu	gcg Ala	1248
				405					410					415		
caa Gln	cat His	gct Ala	gag Glu	caa Gln	cgc Arg	cca Pro	ctg Leu	cgt Arg	cag Gln	cac His	ctg Leu	gtc Val	gcg Ala	ctg Leu	cat His	1296
			420					425					430			
gga Gly	cag Gln	att Ile	gtt Val	ccc Pro	caa Gln	caa Gln	aaa Lys	cgt Arg	ctg Leu	gcg Ala	cag Gln	tta Leu	cag Gln	gtc Val	gct Ala	1344
		435					440					445				
atc Ile	cag Gln	aat Asn	gtc Val	acg Thr	caa Gln	gaa Glu	cag Gln	acg Thr	caa Gln	cgt Arg	aac Asn	gcc Ala	gca Ala	ctt Leu	aac Asn	1392
	450					455					460					
gaa Glu	atg Met	cgc Arg	cag Gln	cgt Arg	tat Tyr	aaa Lys	gaa Glu	aag Lys	acg Thr	cag Gln	caa Gln	ctt Leu	gcc Ala	gat Asp	gtg Val	1440
465					470					475					480	
aaa Lys	acc Thr	att Ile	tgc Cys	gag Glu	cag Gln	gaa Glu	gcg Ala	cgc Arg	atc Ile	aaa Lys	acg Thr	ctg Leu	gaa Glu	gct Ala	caa Gln	1488
				485					490					495		
cgt Arg	gca Ala	cag Gln	tta Leu	cag Gln	gcg Ala	ggt Gly	cag Gln	cct Pro	tgc Cys	cca Pro	ctt Leu	tgt Cys	ggt Gly	tcc Ser	acc Thr	1536
			500					505					510			
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		515					520					525				
cag Gln	tct Ser	cga Arg	tta Leu	ctg Leu	gcg Ala	ctg Leu	gaa Glu	aac Asn	gaa Glu	gtt Val	aaa Lys	aag Lys	ctc Leu	ggt Gly	gaa Glu	1632
	530					535					540					
gaa Glu	ggt Gly	gcg Ala	acg Thr	cta Leu	cgt Arg	ggg Gly	caa Gln	ctg Leu	gac Asp	gcc Ala	ata Ile	aca Thr	aag Lys	cag Gln	ctt Leu	1680
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cag Gln	cgt Arg	gat Asp	gaa Glu	aac Asn	gaa Glu	gcg Ala	caa Gln	agc Ser	ctc Leu	cga Arg	caa Gln	gat Asp	gag Glu	caa Gln	gca Ala	1728
				565					570					575		
ctt Leu	act Thr	caa Gln	caa Gln	tgg Trp	caa Gln	gcc Ala	gtc Val	acg Thr	gcc Ala	agc Ser	ctc Leu	aat Asn	atc Ile	acc Thr	ttg Leu	1776
			580					585					590			

cag Gln	cca Pro	ctg Leu 595	gac Asp	gat Asp	att Ile	caa Gln	ccg Pro 600	tgg Trp	ctg Leu	gat Asp	gca Ala	caa Gln 605	gat Asp	gag Glu	cac His	1824
gaa Glu	cgc Arg 610	cag Gln	ctg Leu	cgg Arg	tta Leu	ctc Leu 615	agc Ser	caa Gln	cgg Arg	cat His	gaa Glu 620	tta Leu	caa Gln	ggg Gly	cag Gln	1872
att Ile 625	gcc Ala	gcg Ala	cat His	aat Asn	cag Gln 630	caa Gln	att Ile	atc Ile	cag Gln	tat Tyr 635	caa Gln	cag Gln	caa Gln	att Ile	gaa Glu 640	1920
caa Gln	cgc Arg	cag Gln	caa Gln	cta Leu 645	ctt Leu	tta Leu	acg Thr	aca Thr	ttg Leu 650	acg Thr	ggt Gly	tat Tyr	gca Ala	ctg Leu 655	aca Thr	1968
ttg Leu	cca Pro	cag Gln 660	gaa Glu	gat Asp	gaa Glu	gaa Glu	gag Glu 665	agc Ser	tgg Trp	ttg Leu	gcg Ala	aca Thr 670	cgt Arg	cag Gln	caa Gln	2016
gaa Glu	gcg Ala 675	cag Gln	agc Ser	tgg Trp	cag Gln	caa Gln	ccg Arg 680	cag Gln	aac Asn	gaa Glu	tta Leu 685	acc Thr	gcg Ala	ctg Leu	caa Gln	2064
aac Asn	cgt Arg 690	att Ile	cag Gln	cag Gln	ctg Leu	acg Thr 695	ccg Pro	att Ile	ctg Leu	gaa Glu 700	acg Thr	ttg Leu	ccg Pro	caa Gln	agt Ser	2112
gat Asp 705	gaa Glu	ctc Leu	ccg Pro	cac His	tgc Cys 710	gaa Glu	gaa Glu	act Thr	gtg Val	gta Val 715	ttg Leu	gaa Glu	aac Asn	tgg Trp 720	cgg Arg	2160
cag Gln	gta Val	cat His	gaa Glu	caa Gln 725	tgt Cys	ctc Leu	gca Ala	tta Leu	cac His 730	agc Ser	cag Gln	cag Gln	cag Gln	acg Thr 735	tta Leu	2208
cag Gln	caa Gln	cag Gln 740	gat Asp	gtt Val	ctg Leu	gcg Ala	gcg Ala	caa Gln 745	agt Ser	ctg Leu	caa Gln	aaa Lys 750	gcc Ala	cag Gln	gcg Ala	2256
cag Gln	ttt Phe 755	gac Asp	acc Thr	gcg Ala	cta Leu	cag Gln	gcc Ala 760	agc Ser	gtc Val	ttt Phe	gac Asp 765	gat Asp	cag Gln	cag Gln	gcg Ala	2304
ttc Phe 770	ctt Leu	gcg Ala	gcg Ala	cta Leu	atg Met 775	gat Asp	gaa Glu	caa Gln	aca Thr	cta Leu 780	acg Thr	cag Gln	ctg Leu	gaa Glu	cag Gln	2352
ctc Leu 785	aag Lys	cag Gln	aat Asn	ctg Leu	gaa Glu 790	aac Asn	cag Gln	cgc Arg	cgt Arg	cag Gln 795	gcg Ala	caa Gln	act Thr	ctg Leu	gtc Val 800	2400
act Thr	cag Gln	aca Thr	gca Ala	gaa Glu 805	acg Thr	ctg Leu	gca Ala	cag Gln	cat His 810	caa Gln	caa Gln	cac His	cga Arg	cct Pro 815	gac Asp	2448

gac Asp	ggg Gly	ttg Leu	gct Ala 820	ctc Leu	act Thr	gtg Val	acg Thr	gtg Val 825	gag Glu	cag Gln	att Ile	cag Gln	caa Gln 830	gag Glu	tta Leu	2496
gcg Ala	caa Gln	act Thr 835	cac His	caa Gln	aag Lys	ttg Leu	cgt Arg 840	gaa Glu	aac Asn	acc Thr	acg Thr 845	agt Ser	caa Gln	ggc Gly	gag Glu	2544
att Ile	cgc Arg 850	cag Gln	cag Gln	ctg Leu	aag Lys 855	cag Gln	gat Asp	gca Ala	gat Asp	aac Asn	cgt Arg 860	cag Gln	caa Gln	caa Gln	caa Gln	2592
acc Thr 865	tta Leu	atg Met	cag Gln	caa Gln 870	att Ile	gct Ala	caa Gln	atg Met	acg Thr 875	cag Gln	cag Gln	gtt Val	gag Glu	gac Asp	tgg Trp 880	2640
gga Gly	tat Tyr	ctg Leu	aat Asn 885	tcg Ser	cta Leu	ata Ile	ggg Gly	tcc Ser 890	aaa Lys	gag Glu	ggc Gly	gat Asp	aaa Lys 895	ttc Phe	cgc Arg	2688
aag Lys	ttt Phe	gcc Ala 900	cag Gln	ggg Gly	ctg Leu	acg Thr	ctg Leu	gat Asp 905	aat Asn	tta Leu	gtc Val	cat His 910	ctc Leu	gct Ala	aat Asn	2736
cag Gln	caa Gln 915	ctt Leu	acc Thr	cgg Arg	ctg Leu	cac His	ggg Gly 920	cgc Arg	tat Tyr	ctg Leu	tta Leu 925	cag Gln	cgc Arg	aaa Lys	gcc Ala	2784
agc Ser	gag Glu 930	gcg Ala	ctg Leu	gaa Glu	gtc Val	gag Glu 935	gtt Val	gtt Val	gat Asp	acc Thr 940	tgg Trp	cag Gln	gca Ala	gat Asp	gcg Ala	2832
gta Val 945	cgc Arg	gat Asp	acc Thr	cgt Arg 950	acc Thr	ctt Leu	tcc Ser	ggc Gly	ggc Gly	gaa Glu 955	agt Ser	ttc Phe	ctc Leu	gtt Val	agt Ser 960	2880
ctg Leu	gcg Ala	ctg Leu	gcg Ala 965	ctg Leu	gcg Ala	ctt Leu	tcg Ser	gat Asp 970	ctg Leu	gtc Val	agc Ser	cat His	aaa Lys 975	aca Thr	cgt Arg	2928
att Ile	gac Asp	tcg Ser 980	ctg Leu	ttc Phe	ctt Leu	gat Asp	gaa Glu 985	ggg Gly	ttt Phe	ggc Gly	acg Thr	ctg Leu 990	gat Asp	agc Ser	gaa Glu	2976
acg Thr	ctg Leu	gat Asp 995	acc Thr	gcc Ala	ctt Leu	gat Asp	gcg Ala 1000	ctg Leu	gat Asp	gcc Ala	ctg Leu 1005	aac Asn	gcc Ala	agt Ser	ggc Gly	3024
aaa Lys	acc Thr 1010	atc Ile	ggg Gly	gtg Val	att Ile	agc Ser 1015	cac His	gta Val	gaa Glu	gcg Ala	atg Met 1020	aaa Lys	gag Glu	cgt Arg	att Ile	3072
ccg Pro 1025	gtg Val	cag Gln	atc Ile	aaa Lys 1030	gtg Val	aaa Lys	aag Lys	atc Ile	aac Asn	ggc Gly 1035	ctg Leu	ggc Gly	tac Tyr	agc Ser	aaa Lys 1040	3120
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1045

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Ser Lys Ser Arg Glu Ala Glu His Gln Ala Phe Leu Asp Trp Leu Leu
20 25 30

gag aca gca caa acc cat cag gtg gat gcg att att gtt gcc ggt gat 144
Glu Thr Ala Gln Thr His Gln Val Asp Ala Ile Ile Val Ala Gly Asp
35 40 45

gtt ttc gat acc ggc tcg ccg ccc agt tac gcc cgc acg tta tac aac 192
Val Phe Asp Thr Gly Ser Pro Pro Ser Tyr Ala Arg Thr Leu Tyr Asn
50 55 60

cgt ttt gtt gtc aat tta cag caa act ggc tgt cat ctg gtg gta ctg 240
Arg Phe Val Val Asn Leu Gln Gln Thr Gly Cys His Leu Val Val Leu
65 70 75 80

gca gga aac cat gac tcg gtc gcc acg ctg aat gaa tcg cgc gat atc 288
Ala Gly Asn His Asp Ser Val Ala Thr Leu Asn Glu Ser Arg Asp Ile
85 90 95

atg gcg ttc ctc aat act acc gtg gtc gcc agc gcc gga cat gcg ccg 336
Met Ala Phe Leu Asn Thr Thr Val Val Ala Ser Ala Gly His Ala Pro
100 105 110

caa atc ttg cct cgt cgc gac ggg acg cca ggc gca gtg ctg tgc ccc 384
Gln Ile Leu Pro Arg Arg Asp Gly Thr Pro Gly Ala Val Leu Cys Pro
115 120 125

att ccg ttt tta cgt ccg cgt gac att att acc agc cag gcg ggg ctt 432
Ile Pro Phe Leu Arg Pro Arg Asp Ile Ile Thr Ser Gln Ala Gly Leu
130 135 140

aac ggt att gaa aaa cag cag cat tta ctg gca gcg att acc gat tat 480
Asn Gly Ile Glu Lys Gln Gln His Leu Leu Ala Ala Ile Thr Asp Tyr
145 150 155 160

tac caa caa cac tat gcc gat gcc tgc aaa ctg cgc gcc gat cag cct 528
Tyr Gln Gln His Tyr Ala Asp Ala Cys Lys Leu Arg Gly Asp Gln Pro
165 170 175

ctg ccc atc atc gcc acg gga cat tta acg acc gtg ggg gcc agt aaa	576
Leu Pro Ile Ile Ala Thr Gly His Leu Thr Thr Val Gly Ala Ser Lys	
180 185 190	
agt gac gcc gtg cgt gac att tat att ggc acg ctg gac gcg ttt ccg	624
Ser Asp Ala Val Arg Asp Ile Tyr Ile Gly Thr Leu Asp Ala Phe Pro	
195 200 205	
gca caa aac ttt cca cca gcc gac tac atc gcg ctc ggg cat att cac	672
Ala Gln Asn Phe Pro Pro Ala Asp Tyr Ile Ala Leu Gly His Ile His	
210 215 220	
cgc gca cag att att ggc ggc atg gaa cat gtt cgc tat tgc ggc tcc	720
Arg Ala Gln Ile Ile Gly Gly Met Glu His Val Arg Tyr Cys Gly Ser	
225 230 235 240	
ccc att cca ctg agt ttt gat gaa tgc ggt aag agt aaa tat gtc cat	768
Pro Ile Pro Leu Ser Phe Asp Glu Cys Gly Lys Ser Lys Tyr Val His	
245 250 255	
ctg gtg aca ttt tca aac ggc aaa tta gag agc gtg gaa aac ctg aac	816
Leu Val Thr Phe Ser Asn Gly Lys Leu Glu Ser Val Glu Asn Leu Asn	
260 265 270	
gta ccg gta acg caa ccc atg gca gtg ctg aaa ggc gat ctg gcg tcg	864
Val Pro Val Thr Gln Pro Met Ala Val Leu Lys Gly Asp Leu Ala Ser	
275 280 285	
att acc gca cag ctg gaa cag tgg cgc gat gta tcg cag gag cca cct	912
Ile Thr Ala Gln Leu Glu Gln Trp Arg Asp Val Ser Gln Glu Pro Pro	
290 295 300	
gtc tgg ctg gat atc gaa atc act act gat gag tat ctg cat gat att	960
Val Trp Leu Asp Ile Glu Ile Thr Thr Asp Glu Tyr Leu His Asp Ile	
305 310 315 320	
cag cgc aaa atc cag gca tta acc gaa tca ttg cct gtc gaa gta ttg	1008
Gln Arg Lys Ile Gln Ala Leu Thr Glu Ser Leu Pro Val Glu Val Leu	
325 330 335	
ctg gta cgt cgg agt cgt gaa cag cgc gag cgt gtg tta gcc agc caa	1056
Leu Val Arg Arg Ser Arg Glu Gln Arg Glu Arg Val Leu Ala Ser Gln	
340 345 350	
cag cgt gaa acc ctc agc gaa ctc agc gtc gaa gag gtg ttc aat cgc	1104
Gln Arg Glu Thr Leu Ser Glu Leu Ser Val Glu Glu Val Phe Asn Arg	
355 360 365	
cgt ctg gca ctg gaa gaa ctg gat gaa tcg cag cag caa cgt ctg cag	1152
Arg Leu Ala Leu Glu Glu Leu Asp Glu Ser Gln Gln Gln Arg Leu Gln	
370 375 380	
cat ctt ttc acc acg acg ttg cat acc ctc gcc gga gaa cac gaa gca	1200
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tga
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1203

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tca gca cag ggc att ggc ttt tta ctg gca acc ggc ctg ggt aaa tat	96
Ser Ala Gln Gly Ile Gly Phe Leu Leu Ala Thr Gly Leu Gly Lys Tyr	
20 25 30	
ggc gca caa ata att att aat gat att act gcc gaa cgc gca gaa ctt	144
Gly Ala Gln Ile Ile Ile Asn Asp Ile Thr Ala Glu Arg Ala Glu Leu	
35 40 45	
gct gta gaa aaa ctc cac cag gag ggt att cag gcc gtt gcc gca cct	192
Ala Val Glu Lys Leu His Gln Glu Gly Ile Gln Ala Val Ala Ala Pro	
50 55 60	
ttt aat gtt act cat aaa cat gaa att gat gcc gcc gtt gaa cat atc	240
Phe Asn Val Thr His Lys His Glu Ile Asp Ala Ala Val Glu His Ile	
65 70 75 80	
gaa aag gac atc ggc ccc att gat gtg ctg gtg aat aac gcc ggt atc	288
Glu Lys Asp Ile Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile	
85 90 95	
cag cgc cgt cat cct ttt act gag ttc cct gaa caa gag tgg aat gat	336
Gln Arg Arg His Pro Phe Thr Glu Phe Pro Glu Gln Glu Trp Asn Asp	
100 105 110	
gtg atc gca gta aac cag acc gcc gtg ttc ctg gta tcg caa gcg gta	384
Val Ile Ala Val Asn Gln Thr Ala Val Phe Leu Val Ser Gln Ala Val	
115 120 125	
act cgt cac atg gtt gaa cgc aag gca ggt aaa gtt att aat att tgc	432
Thr Arg His Met Val Glu Arg Lys Ala Gly Lys Val Ile Asn Ile Cys	
130 135 140	
tcg atg caa agc gaa ctg gga cgt gac acc atc acc cct tat gcc gca	480
Ser Met Gln Ser Glu Leu Gly Arg Asp Thr Ile Thr Pro Tyr Ala Ala	
145 150 155 160	
tcg aaa ggg gcg gta aaa atg ctc acc cgc ggc atg tgc gtc gag ctg	528
Ser Lys Gly Ala Val Lys Met Leu Thr Arg Gly Met Cys Val Glu Leu	

aaa tac tgc att gaa cat aac gag aat cag tgt aca gat atg cgt ttt	336
Lys Tyr Cys Ile Glu His Asn Glu Asn Gln Cys Thr Asp Met Arg Phe	
100 105 110	
ttt ggc agt gcc atg tat ttc cct cat gtt gat ggt ggt ttt acc cgt	384
Phe Gly Ser Ala Met Tyr Phe Pro His Val Asp Gly Gly Phe Thr Arg	
115 120 125	
tat aaa atg gtc gaa acg tcg caa tgt gtc cct tat ccg gcc aaa gct	432
Tyr Lys Met Val Glu Thr Ser Gln Cys Val Pro Tyr Pro Ala Lys Ala	
130 135 140	
gac gaa aag gtt atg gct ttt gcc gaa cct tta gcc gtc gcg att cat	480
Asp Glu Lys Val Met Ala Phe Ala Glu Pro Leu Ala Val Ala Ile His	
145 150 155 160	
gcc gca cat cag gcc ggc gag tta cag ggc aag cga gta ttt att tcc	528
Ala Ala His Gln Ala Gly Glu Leu Gln Gly Lys Arg Val Phe Ile Ser	
165 170 175	
ggg gtt gga ccc att ggc tgc ctg att gtc agt gca gtg aaa aca ctg	576
Gly Val Gly Pro Ile Gly Cys Leu Ile Val Ser Ala Val Lys Thr Leu	
180 185 190	
ggg gcc gcg gaa att gtc tgt gct gat gtg agt ccc cgt tcc ctt tcg	624
Gly Ala Ala Glu Ile Val Cys Ala Asp Val Ser Pro Arg Ser Leu Ser	
195 200 205	
ctg ggc aaa gag atg ggg gcg gat gtg ctc gta aac cca caa aac gac	672
Leu Gly Lys Glu Met Gly Ala Asp Val Leu Val Asn Pro Gln Asn Asp	
210 215 220	
gac atg gat cac tgg aaa gcg gaa aaa ggc tat ttc gat gtc agc ttt	720
Asp Met Asp His Trp Lys Ala Glu Lys Gly Tyr Phe Asp Val Ser Phe	
225 230 235 240	
gaa gtg tcc ggt cat cct tca tca gtg aat acc tgt ctg gag gtc act	768
Glu Val Ser Gly His Pro Ser Ser Val Asn Thr Cys Leu Glu Val Thr	
245 250 255	
cgt gca cgc ggc gta atg gtg cag gta ggt atg gga ggc gcg atg gca	816
Arg Ala Arg Gly Val Met Val Gln Val Gly Met Gly Gly Ala Met Ala	
260 265 270	
gaa ttc cca atg atg acg ttg att ggt aag gag att tca ctc aga ggc	864
Glu Phe Pro Met Met Thr Leu Ile Gly Lys Glu Ile Ser Leu Arg Gly	
275 280 285	
tct ttc cgt ttt acc agc gaa ttt aat acc gca gtg tca tgg ctg gcg	912
Ser Phe Arg Phe Thr Ser Glu Phe Asn Thr Ala Val Ser Trp Leu Ala	
290 295 300	
aat ggc gtt atc aat cca ctg cct tta ctg agt gct gaa tat ccc ttc	960
Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe	
305 310 315 320	

atg ttg cag ccg aag att cag gca atg cgt gag cgt ctg ggc gat gac	1200
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp	
385 390 395 400	
aaa cag cgt atc agc cag gaa atg atg gcg ctg tac aaa gct gag aag	1248
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys	
405 410 415	
gtt aac ccg ctg ggc ggc tgc ttc ccg ctg ctg atc cag atg cca atc	1296
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Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln	
435 440 445	
gca ccg ttt gca ctg tgg atc cac gac ctg tcg gca cag gac ccg tac	1392
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr	
450 455 460	
tac atc ctg ccg atc ctg atg ggc gta acg atg ttc ttc att cag aag	1440
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys	
465 470 475 480	
atg tcg ccg acc aca gtg acc gac ccg atg cag cag aag atc atg acc	1488
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr	
485 490 495	
ttt atg ccg gtc atc ttc acc gtg ttc ttc ctg tgg ttc ccg tca ggt	1536
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly	
500 505 510	
ctg gtg ctg tac tat atc gtc agc aac ctg gta acc att att cag cag	1584
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln	
515 520 525	
cag ctg att tac cgt ggt ctg gaa aaa cgt ggc ctg cat agc cgc gag	1632
Gln Leu Ile Tyr Arg Gly Leu Glu Lys Arg Gly Leu His Ser Arg Glu	
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Lys Lys Lys Ser *	
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 <213> Escherichia coli

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ggc Gly	gca Ala	acg Thr	gga Gly 20	gcc Ala	ggg Gly	att Ile	gcc Ala	cgc Arg 25	gac Asp	tgt Cys	gcc Ala	ctg Leu	cgc Arg 30	ggg Gly	ctg Leu	96
cgc Arg	gtg Val 35	att Ile	ttg Leu	gtt Val	gag Glu	cgc Arg 40	cac His	gac Asp	atc Ile	gca Ala	acc Thr 45	ggg Gly	gcc Ala	acc Thr	ggg Gly	144
cgt Arg 50	aac Asn	cac His	ggc Gly	ctg Leu	ctg Leu	cac His 55	agc Ser	ggg Gly	gca Ala	cgc Arg 60	tat Tyr	gca Ala	gta Val	acc Thr	gat Asp	192
gca Ala 65	gaa Glu	tcg Ser	gcc Ala	cgc Arg	gaa Glu 70	tgc Cys	att Ile	agt Ser	gaa Glu	aac Asn 75	cag Gln	atc Ile	ctg Leu	aaa Lys	cgc Arg 80	240
att Ile	gca Ala	cgt Arg	cac His 85	tgc Cys	gtt Val	gaa Glu	cca Pro	acc Thr 90	aac Asn	ggc Gly	ctg Leu	ttt Phe	atc Ile 95	acc Thr	ctg Leu	288
ccg Pro	gaa Glu	gat Asp 100	gac Asp	ctc Leu	tcc Ser	ttc Phe	cag Gln	gcc Ala 105	act Thr	ttt Phe	att Ile	cgc Arg 110	gcc Ala	tgc Cys	gaa Glu	336
gaa Glu	gca Ala 115	ggg Gly	atc Ile	agc Ser	gca Ala	gaa Glu 120	gct Ala	ata Ile	gac Asp	ccg Pro	cag Gln	caa Gln 125	gca Ala	cgc Arg	att Ile	384
atc Ile 130	gaa Glu	cct Pro	gcc Ala	gtt Val	aac Asn	ccg Pro 135	gca Ala	ctg Leu	att Ile	ggc Gly 140	gca Ala	gtg Val	aaa Lys	gtt Val	ccg Pro	432
gat Asp 145	ggc Gly	acc Thr	gtt Val	gat Asp 150	cca Pro	ttt Phe	cgt Arg	ctg Leu	acc Thr	gca Ala 155	gca Ala	aac Asn	atg Met	ctg Leu	gat Asp 160	480
gcc Ala	aaa Lys	gaa Glu	cac His 165	ggg Gly	gcc Ala	gtt Val	atc Ile	ctt Leu	acc Thr 170	gct Ala	cat His	gaa Glu	gtc Val	acc Thr 175	ggg Gly	528
ctg Leu	att Ile	cgt Arg	gaa Glu 180	ggc Gly	gca Ala	acg Thr	gtg Val	tgc Cys 185	ggg Gly	gtt Val	cgt Arg	gta Val	cgt Arg 190	aac Asn	cat His	576
ctc Leu	acc Thr 195	ggc Gly	gaa Glu	act Thr	cag Gln	gcc Ala	ctt Leu 200	cat His	gca Ala	cct Pro	gtc Val	gtg Val	gtt Val 205	aat Asn	gcc Ala	624
gct Ala 210	ggg Gly	atc Ile	tgg Trp	ggg Gly	caa Gln	cac His 215	att Ile	gcc Ala	gaa Glu	tat Tyr 220	gcc Ala	gat Asp	ctg Leu	cgc Arg	att Ile	672
cgc Arg	atg Met	ttc Phe	ccg Pro	gca Ala	aaa Lys	gga Gly	tcg Ser	ctg Leu	ctg Leu	atc Ile	atg Met	gat Asp	cac His	cgc Arg	att Ile	720

gtg	ggg	atg	ggc	acc	tgc	cag	ggc	gaa	ctc	tgc	gcc	tgc	cgc	gct	gcc	1440
Val	Gly	Met	Gly	Thr	Cys	Gln	Gly	Glu	Leu	Cys	Ala	Cys	Arg	Ala	Ala	
465					470					475					480	
gga	ctg	ctg	caa	cgt	ttt	aac	gtc	acg	acg	tcc	gcg	caa	tct	atc	gag	1488
Gly	Leu	Leu	Gln	Arg	Phe	Asn	Val	Thr	Thr	Ser	Ala	Gln	Ser	Ile	Glu	
				485					490					495		
caa	ctt	tcc	acc	ttc	ctt	aac	gaa	cgc	tgg	aaa	ggc	gtg	caa	ccc	atc	1536
Gln	Leu	Ser	Thr	Phe	Leu	Asn	Glu	Arg	Trp	Lys	Gly	Val	Gln	Pro	Ile	
			500					505					510			
gcc	tgg	gga	gat	gca	ctg	cgc	gaa	agc	gaa	ttt	acc	cgc	tgg	gtt	tat	1584
Ala	Trp	Gly	Asp	Ala	Leu	Arg	Glu	Ser	Glu	Phe	Thr	Arg	Trp	Val	Tyr	
		515					520					525				
cag	gga	ttg	tgt	ggc	ctg	gag	aag	gag	cag	aaa	gat	gcg	ctt	tga		1629
Gln	Gly	Leu	Cys	Gly	Leu	Glu	Lys	Glu	Gln	Lys	Asp	Ala	Leu	*		
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<212> DNA
<213> Escherichia coli
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<221> CDS
<222> (1)...(1260)
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Met	Arg	Phe	Asp	Thr	Val	Ile	Met	Gly	Gly	Gly	Leu	Ala	Gly	Leu	Leu	
1				5				10						15		
tgt	ggc	ctg	caa	ctg	caa	aaa	cac	ggc	ctg	cgc	tgt	gcc	att	gtc	act	96
Cys	Gly	Leu	Gln	Leu	Gln	Lys	His	Gly	Leu	Arg	Cys	Ala	Ile	Val	Thr	
		20						25				30				
cgt	ggg	caa	agc	gca	ctg	cat	ttc	tca	tcc	gga	tcg	ctg	gat	ttg	ctg	144
Arg	Gly	Gln	Ser	Ala	Leu	His	Phe	Ser	Ser	Gly	Ser	Leu	Asp	Leu	Leu	
		35				40						45				
agc	cat	ctg	cca	gat	ggg	caa	ccg	gtg	aca	gac	att	cac	agt	gga	ctg	192
Ser	His	Leu	Pro	Asp	Gly	Gln	Pro	Val	Thr	Asp	Ile	His	Ser	Gly	Leu	
50						55				60						
gaa	tct	ttg	cgt	cag	cag	gca	cca	gcc	cat	cct	tac	tcc	ctt	ctc	gag	240
Glu	Ser	Leu	Arg	Gln	Gln	Ala	Pro	Ala	His	Pro	Tyr	Ser	Leu	Leu	Glu	
65				70						75				80		
cca	caa	cgc	gtg	ctc	gat	ctc	gct	tgc	cag	gcg	cag	gca	tta	atc	gct	288
Pro	Gln	Arg	Val	Leu	Asp	Leu	Ala	Cys	Gln	Ala	Gln	Ala	Leu	Ile	Ala	
				85				90						95		

gcg Ala	aaa Lys	tat Tyr	gac Asp	acc Thr 85	acg Thr	cgc Arg	ccg Pro	tcg Ser	ctg Leu 90	cgt Arg	aat Asn	ttt Phe	gtg Val	ttg Leu 95	agt Ser	288
cat His	acc Thr	gac Asp	ctg Leu 100	atg Met	ggg Gly	agc Ser	gtt Val	tcc Ser 105	acg Thr	ccg Pro	ttc Phe	gca Ala	cca Pro 110	atc Ile	gtc Val	336
aac Asn	acc Thr	gct Ala 115	acc Thr	tcg Ser	ctg Leu	aaa Lys	ccg Pro 120	gtg Val	cgg Arg	cag Gln	ctg Leu 125	ctt Leu	gat Asp	gcg Ala	gcg Ala	384
tta Leu	aaa Lys 130	atc Ile	gat Asp	cat His	cgc Arg	cgc Arg	acg Thr 135	cta Leu	ccg Pro	aaa Lys 140	tac Tyr	tcc Ser	ttc Phe	ggc Gly	acg Thr	432
ttc Phe 145	cgt Arg	cgc Arg	tgg Trp	tat Tyr	cgc Arg 150	agc Ser	gtg Val	gcg Ala	gct Ala 155	cag Gln	caa Gln	gca Ala	caa Gln	tat Tyr	aaa Lys 160	480
gac Asp	cag Gln	gtc Val	gct Ala 165	ttc Phe	ttt Phe	cac His	ggc Gly	tgc Cys 170	ttc Phe	gtt Val	aac Asn	tac Tyr	aac Asn 175	cat His	ccg Pro	528
cag Gln	tta Leu	ggg Gly	aaa Lys 180	gat Asp	tta Leu	att Ile	aaa Lys	gtg Val 185	ctc Leu	aac Asn	gca Ala	atg Met	ggg Gly 190	acc Thr	ggg Gly	576
gta Val	caa Gln 195	ctg Leu	ctc Leu	agc Ser	aaa Lys	gaa Glu	aaa Lys 200	tgc Cys	tgc Cys	ggc Gly	gta Val 205	ccg Pro	cta Leu	atc Ile	gcc Ala	624
aac Asn	ggc Gly 210	ttt Phe	acc Thr	gat Asp	aaa Lys	gca Ala 215	cgc Arg	aaa Lys	cag Gln	gca Ala 220	att Ile	acg Thr	aat Asn	gta Val	gag Glu	672
tcg Ser 225	atc Ile	cgc Arg	gaa Glu	gct Ala	gtg Val 230	gga Gly	gta Val	aaa Lys	ggc Gly 235	att Ile	ccg Pro	gtg Val	att Ile	gcc Ala	acc Thr 240	720
tcc Ser	tca Ser	acc Thr	tgt Cys 245	aca Thr	ttt Phe	gcc Ala	ctg Leu	cgc Arg	gac Asp 250	gaa Glu	tac Tyr	ccg Pro	gaa Glu	gtg Val 255	ctg Leu	768
aat Asn	gtc Val	gac Asp	aac Asn 260	aaa Lys	ggc Gly	ttg Leu	cgc Arg	gat Asp 265	cat His	atc Ile	gaa Glu	ctg Leu 270	gca Ala	acc Thr	cgc Arg	816
tgg Trp	ctg Leu	tgg Trp 275	cgc Arg	aag Lys	ctg Leu	gac Asp	gaa Glu 280	ggc Gly	aaa Lys	acg Thr	tta Leu 285	ccg Pro	ctg Leu	aaa Lys	ccg Pro	864
ctg Leu	ccg Pro 290	ctg Leu	aaa Lys	gtg Val	gtt Val	tat Tyr 295	cac His	act Thr	ccg Pro	tgc Cys 300	cat His	atg Met	gaa Glu	aaa Lys	atg Met	912

ggc tgg acg ctc tac acc ctg gag ctg ttg cgt aac atc ccg ggg ctt 960
 Gly Trp Thr Leu Tyr Thr Leu Glu Leu Leu Arg Asn Ile Pro Gly Leu
 305 310 315 320

gag tta acg gtg ctg gat tcc cag tgc tgc ggt att gcg ggt act tac 1008
 Glu Leu Thr Val Leu Asp Ser Gln Cys Cys Gly Ile Ala Gly Thr Tyr
 325 330 335

ggg ttc aaa aaa gag aac tac ccc acc tca caa gcc atc ggc gca cca 1056
 Gly Phe Lys Lys Glu Asn Tyr Pro Thr Ser Gln Ala Ile Gly Ala Pro
 340 345 350

ctg ttc cgc cag ata gaa gaa agc ggc gca gat ctg gtg gtc acc gac 1104
 Leu Phe Arg Gln Ile Glu Glu Ser Gly Ala Asp Leu Val Val Thr Asp
 355 360 365

tgc gaa acc tgt aaa tgg cag att gag atg tcc aca agt ctt cgc tgc 1152
 Cys Glu Thr Cys Lys Trp Gln Ile Glu Met Ser Thr Ser Leu Arg Cys
 370 375 380

gaa cat ccg att acg cta ctg gcc cag gcg ctg gct taa 1191
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 385 390 395

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 <213> Escherichia coli

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gca gga ctg gca cag gca gat gac gcc gcc ccg gca gcg ggc agt act 96
 Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
 20 25 30

ctg gac aaa atc gcc aaa aac ggt gtg att gtc gtc ggt cac cgt gaa 144
 Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
 35 40 45

tct tca gtg cct ttc tct tat tac gac aat cag caa aaa gtg gtg ggt 192
 Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
 50 55 60

tac tcg cag gat tac tcc aac gcc att gtt gaa gca gtg aaa aag aaa 240
 Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
 65 70 75 80

ctc aac aaa ccg gac ttg cag gta aaa ctg att ccg att acc tca caa 288
 Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln

	85	90	95	
aac cgt att cca ctg ctg caa aac ggc act ttc gat ttt gaa tgt ggt				336
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly	100	105	110	
tct acc acc aac aac gtc gaa cgc caa aaa cag gcg gct ttc tct gac				384
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp	115	120	125	
act att ttc gtg gtc ggt acg cgc ctg ttg acc aaa aag ggt ggc gat				432
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp	130	135	140	
atc aaa gat ttt gcc aac ctg aaa gac aaa gcc gta gtc gtc act tcc				480
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser	145	150	155	160
ggc act acc tct gaa gtt ttg ctc aac aaa ctg aat gaa gag caa aaa				528
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys	165	170	175	
atg aat atg cgc atc atc agc gcc aaa gat cac ggt gac tct ttc cgc				576
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg	180	185	190	
acc ctg gaa agc ggt cgt gcc gtt gcc ttt atg atg gat gac gct ctg				624
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu	195	200	205	
ctg gcc ggt gaa cgt gcg aaa gcg aag aaa cca gac aac tgg gaa atc				672
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile	210	215	220	
gtc gcc aag ccg cag tct cag gag gcc tac ggt tgt atg ttg cgt aaa				720
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys	225	230	235	240
gat gat ccg cag ttc aaa aag ctg atg gat gac acc atc gct cag gtg				768
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val	245	250	255	
cag acc tcc ggt gaa gcg gaa aaa tgg ttt gat aag tgg ttc aaa aat				816
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn	260	265	270	
cca att ccg ccg aaa aac ctg aac atg aat ttc gaa ctg tca gac gaa				864
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu	275	280	285	
atg aaa gca ctg ttc aaa gaa ccg aat gac aag gca ctg aac taa				909
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn *	290	295	300	

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1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala
50 55 60

gat caa atc ctc gaa gaa cat caa ttt gcg ttg cag ctg gta aat gat 240
Asp Gln Ile Leu Glu Glu His Gln Phe Ala Leu Gln Leu Val Asn Asp
65 70 75 80

gaa gtt ccg gtc gca gca cct gtg gcc ttt aac ggt cag act tta ttg 288
Glu Val Pro Val Ala Ala Pro Val Ala Phe Asn Gly Gln Thr Leu Leu
85 90 95

aat cat cag gga ttt tat ttc gct gtt ttt cca agc gtc ggt ggt cgc 336
Asn His Gln Gly Phe Tyr Phe Ala Val Phe Pro Ser Val Gly Gly Arg
100 105 110

cag ttc gaa gct gat aat atc gat cag atg gaa gcg gtt ggg cgt tat 384
Gln Phe Glu Ala Asp Asn Ile Asp Gln Met Glu Ala Val Gly Arg Tyr
115 120 125

tta	ggg	cgt	atg	cac	cag	acg	ggg	cgc	aaa	cag	ctt	ttt	atc	cat	cgc	432
Leu	Gly	Arg	Met	His	Gln	Thr	Gly	Arg	Lys	Gln	Leu	Phe	Ile	His	Arg	
	130					135					140					

ccg acc atc ggt ttg aac gaa tat ctc att gag cca cgc aag ctg ttt 480
Pro Thr Ile Gly Leu Asn Glu Tyr Leu Ile Glu Pro Arg Lys Leu Phe
145 150 155 160

gag gac gct aca ctg ata cct tcc ggg ttg aaa gcg gca ttc ctg aaa 528
Glu Asp Ala Thr Leu Ile Pro Ser Gly Leu Lys Ala Ala Phe Leu Lys
165 170 175

gcg aca gat gag ctg att gcc gcc gtt aca gca cac tgg cgg gaa gat 576
Ala Thr Asp Glu Leu Ile Ala Ala Val Thr Ala His Trp Arg Glu Asp
180 185 190

ttc acc gtt ctg cgg cta cat gga gac tgc cac gcc ggg aat att ctc	624
Phe Thr Val Leu Arg Leu His Gly Asp Cys His Ala Gly Asn Ile Leu	
195 200 205	
tggt cgc gat ggt cca atg ttt gtt gat ctg gat gat gca cgt aat ggt	672
Trp Arg Asp Gly Pro Met Phe Val Asp Leu Asp Asp Ala Arg Asn Gly	
210 215 220	
cca gcc gtt cag gat ttg tgg atg ttg ctc aat ggc gat aaa gcc gag	720
Pro Ala Val Gln Asp Leu Trp Met Leu Leu Asn Gly Asp Lys Ala Glu	
225 230 235 240	
cag cgg atg caa ctg gaa act att att gaa gct tat gaa gaa ttt agc	768
Gln Arg Met Gln Leu Glu Thr Ile Ile Glu Ala Tyr Glu Glu Phe Ser	
245 250 255	
gag ttc gac acc gct gaa atc gga ctg att gaa cct tta cgc gcc atg	816
Glu Phe Asp Thr Ala Glu Ile Gly Leu Ile Glu Pro Leu Arg Ala Met	
260 265 270	
cgt ttg gtt tat tat ctt gcc tgg cta atg cgg cgt tgg gct gat ccc	864
Arg Leu Val Tyr Tyr Leu Ala Trp Leu Met Arg Arg Trp Ala Asp Pro	
275 280 285	
gcg ttc ccg aaa aat ttc ccg tgg tta acc ggg gaa gat tac tgg ctg	912
Ala Phe Pro Lys Asn Phe Pro Trp Leu Thr Gly Glu Asp Tyr Trp Leu	
290 295 300	
cga cag acg gcg act ttt ata gaa cag gca aaa gtt cta caa gaa ccc	960
Arg Gln Thr Ala Thr Phe Ile Glu Gln Ala Lys Val Leu Gln Glu Pro	
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cct ttg caa tta aca cct atg tat taa	987
Pro Leu Gln Leu Thr Pro Met Tyr *	
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1 5 10 15	
gca tcg gcg gcg cag tat gaa gat ggt aaa cag tac act acc ctg gaa	96
Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu	
20 25 30	
aaa ccg gta gct ggc gcg ccg caa gtg ctg gag ttt ttc tct ttc ttc	144
Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe	

50				55				60								
att Ile 65	gat Asp	gcg Ala	gtg Val	gga Gly	tcc Ser 70	ggg Gly	gtt Val	gat Asp	gat Asp	tta Leu 75	cac His	cct Pro	ggc Gly	gat Asp	gcg Ala 80	240
gtt Val	gcc Ala	tgt Cys	gtg Val	ccg Pro 85	tta Leu	tta Leu	ccc Pro	tgt Cys	ttt Phe 90	act Thr	tgt Cys	cca Pro	gag Glu	tgt Cys 95	ctg Leu	288
aaa Lys	ggg Gly	ttt Phe	tat Tyr 100	tcc Ser	cag Gln	tgc Cys	gca Ala	aaa Lys 105	tat Tyr	gat Asp	ttt Phe	att Ile	ggc Gly 110	tcg Ser	cgg Arg	336
cgt Arg	gat Asp	ggg Gly 115	gga Gly	ttt Phe	gct Ala	gaa Glu	tat Tyr 120	att Ile	gtc Val	gtt Val	aag Lys	cga Arg 125	aaa Lys	aat Asn	gtc Val	384
ttt Phe 130	gct Ala	cta Leu	ccc Pro	acg Thr	gat Asp	atg Met 135	cct Pro	att Ile	gag Glu	gat Asp	ggg Gly 140	gct Ala	ttt Phe	att Ile	gag Glu	432
ccg Pro 145	att Ile	acc Thr	gtt Val	ggg Gly	ctg Leu 150	cat His	gct Ala	ttt Phe	cat His	tta Leu 155	gcg Ala	caa Gln	ggg Gly	tgt Cys	gag Glu 160	480
aat Asn	aaa Lys	aac Asn	gtt Val	att Ile 165	att Ile	att Ile	ggg Gly	gcc Ala 170	gga Gly	acc Thr	att Ile	ggc Gly	ctg Leu 175	ctg Leu	gcc Ala	528
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att Ile	agt Ser	tca Ser 195	gaa Glu	aaa Lys	ctg Leu	gca Ala	ctg Leu 200	gca Ala	aaa Lys	tct Ser	ttc Phe	ggg Gly 205	gcg Ala	atg Met	caa Gln	624
aca Thr 210	ttt Phe	aac Asn	agt Ser	agc Ser	gaa Glu	atg Met 215	agc Ser	gcg Ala	ccg Pro	caa Gln	atg Met 220	cag Gln	agc Ser	gtt Val	tta Leu	672
cgc Arg 225	gaa Glu	ctg Leu	cgc Arg	ttt Phe	aat Asn 230	cag Gln	ctt Leu	atc Ile	ctc Leu	gag Glu 235	acg Thr	gct Ala	ggc Gly	gta Val	ccg Pro 240	720
caa Gln	act Thr	gtc Val	gaa Glu	ctg Leu 245	gcg Ala	gta Val	gag Glu	att Ile	gcc Ala 250	ggg Gly	cct Pro	cat His	gcc Ala	caa Gln 255	ctg Leu	768
gcg Ala	ctg Leu	gtg Val	ggc Gly 260	acg Thr	ttg Leu	cat His	cag Gln	gat Asp 265	ctg Leu	cat His	tta Leu	aca Thr	tcg Ser 270	gca Ala	acg Thr	816
ttt Phe	ggc Gly 275	aaa Lys	ata Ile	ttg Leu	cgt Arg	aaa Lys 280	gag Glu	ctg Leu	acg Thr	gtt Val	atc Ile 285	ggc Gly	agt Ser	tgg Trp	atg Met	864

aac tac tcc agc cct tgg ccg ggg cag gag tgg gaa acg gcg agc cgg 912
 Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
 290 295 300
 ttg ctg aca gaa cgt aag tta agc ctg gag cca tta atc gct cac cgt 960
 Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
 305 310 315 320
 gga agc ttt gaa agc ttc gcc cag gcg gtg cgt gac atc gct cgt aat 1008
 Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
 325 330 335
 gct atg ccg ggc aaa gtg ttg ctc att ccc tga 1041
 Ala Met Pro Gly Lys Val Leu Leu Ile Pro *
 340 345

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 <213> Escherichia coli

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 1 5 10 15
 atg ctg ccg att gtc atc att att ttt tct aaa ata tta ggc atg aag 96
 Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
 20 25 30
 gca ggc gat tgc ttt aaa gcg ggt ctg cat atc ggg att ggc ttt gtt 144
 Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
 35 40 45
 ggc att ggc ctt gtg att ggc tta atg ctg gat tcc att ggc ccg gcg 192
 Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
 50 55 60
 gcg aaa gcg atg gcg gaa aat ttc gac ctg aat ctg cat gtg gtc gat 240
 Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
 65 70 75 80
 gtt ggc tgg ccg ggc tct tca cca atg acc tgg gcg tcg caa att gcg 288
 Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
 85 90 95
 ctg gtg gcg att ccg att gcg att ctg gtt aac gtg gcg atg tta ctg 336
 Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
 100 105 110
 acc cgt atg acg ccg gtg gta aat gtt gat atc tgg aat atc tgg cat 384

Thr	Arg	Met	Thr	Arg	Val	Val	Asn	Val	Asp	Ile	Trp	Asn	Ile	Trp	His		
		115					120					125					
atg	acc	ttc	acc	ggc	gcg	ttg	ctg	cat	ctg	gca	acc	ggg	tca	tgg	atg	432	
Met	Thr	Phe	Thr	Gly	Ala	Leu	Leu	His	Leu	Ala	Thr	Gly	Ser	Trp	Met		
		130				135					140						
ata	ggg	atg	gca	ggg	gtg	gta	att	cac	gcg	gcg	ttt	gtt	tat	aag	ctc	480	
Ile	Gly	Met	Ala	Gly	Val	Val	Ile	His	Ala	Ala	Phe	Val	Tyr	Lys	Leu		
		145			150					155					160		
ggc	gac	tgg	ttt	gcc	cgc	gat	acc	cga	aat	ttc	ttt	gag	ctg	gaa	ggg	528	
Gly	Asp	Trp	Phe	Ala	Arg	Asp	Thr	Arg	Asn	Phe	Phe	Glu	Leu	Glu	Gly		
			165						170					175			
att	gct	att	ccg	cac	ggg	acg	tcg	gcg	tat	atg	ggg	ccg	att	gcg	gtg	576	
Ile	Ala	Ile	Pro	His	Gly	Thr	Ser	Ala	Tyr	Met	Gly	Pro	Ile	Ala	Val		
			180					185						190			
ctg	gtc	gat	gct	atc	atc	gag	aaa	atc	cca	ggc	gtt	aac	cga	att	aaa	624	
Leu	Val	Asp	Ala	Ile	Ile	Glu	Lys	Ile	Pro	Gly	Val	Asn	Arg	Ile	Lys		
		195					200					205					
ttt	agc	gcc	gac	gat	att	cag	cgc	aaa	ttt	ggg	cca	ttt	ggc	gag	cct	672	
Phe	Ser	Ala	Asp	Asp	Ile	Gln	Arg	Lys	Phe	Gly	Pro	Phe	Gly	Glu	Pro		
		210				215					220						
gtc	acc	gtg	ggg	ttt	gtg	atg	ggg	ctg	att	atc	ggc	atc	ctc	gcg	ggg	720	
Val	Thr	Val	Gly	Phe	Val	Met	Gly	Leu	Ile	Ile	Gly	Ile	Leu	Ala	Gly		
		225			230					235					240		
tac	gat	gtc	aaa	ggg	gta	ttg	cag	ctg	gcg	gta	aaa	acg	gcg	gca	gtg	768	
Tyr	Asp	Val	Lys	Gly	Val	Leu	Gln	Leu	Ala	Val	Lys	Thr	Ala	Ala	Val		
			245						250					255			
atg	ctg	cta	atg	cca	cgg	gtg	att	aaa	ccc	atc	atg	gat	ggg	tta	acg	816	
Met	Leu	Leu	Met	Pro	Arg	Val	Ile	Lys	Pro	Ile	Met	Asp	Gly	Leu	Thr		
			260					265					270				
ccc	atc	gct	aag	cag	gct	cgt	agt	cgt	tta	cag	gcg	aag	ttc	ggc	ggg	864	
Pro	Ile	Ala	Lys	Gln	Ala	Arg	Ser	Arg	Leu	Gln	Ala	Lys	Phe	Gly	Gly		
		275					280					285					
cag	gag	ttc	ctg	att	ggc	ctt	gat	ccg	gcg	ttg	ctg	ctg	gga	cat	acg	912	
Gln	Glu	Phe	Leu	Ile	Gly	Leu	Asp	Pro	Ala	Leu	Leu	Leu	Gly	His	Thr		
		290				295					300						
gcg	gtg	gta	tcg	gca	agc	ctg	att	ttt	atc	cca	ctc	acc	att	tta	att	960	
Ala	Val	Val	Ser	Ala	Ser	Leu	Ile	Phe	Ile	Pro	Leu	Thr	Ile	Leu	Ile		
		305			310					315					320		
gct	gtt	tgt	gtg	ccg	ggg	aat	cag	gtg	ctg	ccg	ttt	ggc	gat	ctt	gcc	1008	
Ala	Val	Cys	Val	Pro	Gly	Asn	Gln	Val	Leu	Pro	Phe	Gly	Asp	Leu	Ala		
				325				330						335			
acc	atc	ggc	ttc	ttc	gtg	gcg	atg	gcg	gtc	gcc	gtg	cat	cgt	gga	aat	1056	
Thr	Ile	Gly	Phe	Phe	Val	Ala	Met	Ala	Val	Ala	Val	His	Arg	Gly	Asn		

	ctg	ttc	cgc	acc	tta	atc	tcg	ggg	gtc	atc	att	atg	agc	atc	acc	ctg	1104
	Leu	Phe	Arg	Thr	Leu	Ile	Ser	Gly	Val	Ile	Ile	Met	Ser	Ile	Thr	Leu	
			355					360					365				
	tgg	atc	gcg	acg	caa	act	att	ggg	ttg	cac	acc	caa	ctg	gcg	gct	aat	1152
	Trp	Ile	Ala	Thr	Gln	Thr	Ile	Gly	Leu	His	Thr	Gln	Leu	Ala	Ala	Asn	
		370					375					380					
	gct	ggg	gcg	tta	aaa	gcc	ggg	ggg	atg	gtg	gct	tca	atg	gat	cag	ggc	1200
	Ala	Gly	Ala	Leu	Lys	Ala	Gly	Gly	Met	Val	Ala	Ser	Met	Asp	Gln	Gly	
	385					390					395					400	
	ggg	tct	ccc	att	acc	tgg	tta	ctg	att	cag	gtt	ttc	tcc	ccg	caa	aat	1248
	Gly	Ser	Pro	Ile	Thr	Trp	Leu	Leu	Ile	Gln	Val	Phe	Ser	Pro	Gln	Asn	
					405					410					415		
	att	ccc	ggg	ttc	att	att	atc	ggg	gca	att	tat	ctg	acc	ggg	att	ttc	1296
	Ile	Pro	Gly	Phe	Ile	Ile	Ile	Gly	Ala	Ile	Tyr	Leu	Thr	Gly	Ile	Phe	
				420				425						430			
	atg	acc	tgg	cgt	aga	gcg	cgt	ggc	ttt	att	aaa	caa	gag	aaa	gtc	ggt	1344
	Met	Thr	Trp	Arg	Arg	Ala	Arg	Gly	Phe	Ile	Lys	Gln	Glu	Lys	Val	Val	
			435					440					445				
	ctc	gca	gaa	ttaa													1356
	Leu	Ala	Glu	*													
			450														
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	Met	Lys	Arg	Lys	Ile	Ile	Val	Ala	Cys	Gly	Gly	Ala	Val	Ala	Thr	Ser	
	1				5					10					15		
	acg	atg	gcg	gcg	gaa	gaa	att	aaa	gag	ttg	tgt	cag	aat	cat	aat	att	96
	Thr	Met	Ala	Ala	Glu	Glu	Ile	Lys	Glu	Leu	Cys	Gln	Asn	His	Asn	Ile	
				20					25					30			
	cct	gtt	gaa	tta	atc	cag	tgt	cgg	gtt	aat	gaa	ata	gaa	acc	tat	atg	144
	Pro	Val	Glu	Leu	Ile	Gln	Cys	Arg	Val	Asn	Glu	Ile	Glu	Thr	Tyr	Met	
			35					40					45				
	gat	ggg	gtg	cat	ttg	ata	tgc	acc	act	gcc	aaa	gtg	gat	cgt	agt	ttt	192
	Asp	Gly	Val	His	Leu	Ile	Cys	Thr	Thr	Ala							

Val Leu Asp Ser Asp Glu *
145 150

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<211> 1263
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1263)

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Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
1 5 10 15

tgt tca gtc tgt tct gcc cat ccg ttg gtt atc gaa gcg gcg ctg gca 96
Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
20 25 30

ttt gat cgc aac agc acg cgc aaa gtg ctg att gaa gca acg tca aac 144
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
35 40 45

cag gtc aat caa ttt ggc ggt tat acc gga atg aca ccg gca gac ttt 192
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
50 55 60

cgc gaa ttt gtt ttt acg att gcc gat aaa gtt ggg ttt gca cgc gaa 240
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
65 70 75 80

cgc att att ctc ggc ggc gat cat ctg ggg cca aac tgc tgg cag caa 288
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
85 90 95

gaa aat gcg gat gcg gcg atg gaa aaa tcc gtc gag ctg gta aag gaa 336
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
100 105 110

tat gtt cgt gcc ggc ttc agt aaa att cat ctt gat gcg tca atg tcc 384
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
115 120 125

tgc gcg ggg gat ccc ata ccg tta gca cca gaa acg gtt gcg gaa cga 432
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
130 135 140

gct gct gtg ctt tgc ttt gct gcg gaa agt gtg gcg aca gat tgc cag 480
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
145 150 155 160

cgt gag caa ctg agc tat gtc att ggc acc gaa gtt ccg gtt ccg ggc 528
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly
165 170 175

ggt Gly	gag Glu	gcc Ala	agc Ser 180	gcc Ala	att Ile	cag Gln	tca Ser	gta Val 185	cac His	atc Ile	acc Thr	cat His	gtt Val 190	gaa Glu	gat Asp	576
gcc Ala	gcc Ala	aat Asn 195	act Thr	tta Leu	cgt Arg	acg Thr	cat His 200	caa Gln	aag Lys	gcc Ala	ttt Phe 205	att Ile	gcc Ala	cgt Arg	ggg Gly	624
ctg Leu	aca Thr 210	gag Glu	gcg Ala	tta Leu	aca Thr	cgt Arg 215	gtg Val	att Ile	gcc Ala	atc Ile	gtg Val 220	gtg Val	cag Gln	ccg Pro	ggt Gly	672
gtg Val 225	gaa Glu	ttt Phe	gat Asp	cac His	agc Ser 230	aat Asn	att Ile	atc Ile	cat His	tat Tyr 235	cag Gln	ccg Pro	cag Gln	gaa Glu	gcg Ala 240	720
cag Gln	ccg Pro	ctg Leu	gcg Ala	caa Gln 245	tgg Trp	ata Ile	gaa Glu	aac Asn 250	acc Thr	cga Arg	atg Met	gtt Val	tat Tyr	gaa Glu 255	gca Ala	768
cat His	tct Ser	acc Thr 260	gat Asp	tac Tyr	cag Gln	acc Thr	cgg Arg 265	acg Thr	gct Ala	tat Tyr	tgg Trp	gaa Glu 270	tta Leu	gtc Val	cgc Arg	816
gat Asp	cac His	ttt Phe 275	gca Ala	ata Ile	ttg Leu	aaa Lys	gtc Val 280	ggt Gly	ccc Pro	gca Ala	tta Leu	acc Thr 285	ttt Phe	gct Ala	tta Leu	864
cgc Arg 290	gag Glu	gcg Ala	ata Ile	ttt Phe	gca Ala	ctg Leu 295	gca Ala	caa Gln	att Ile	gag Glu	cag Gln 300	gaa Glu	ctt Leu	atc Ile	gcc Ala	912
cct Pro 305	gaa Glu	aat Asn	cgc Arg	agc Ser	ggt Gly 310	tgc Cys	ctg Leu	gcg Ala	gta Val	att Ile 315	gaa Glu	gaa Glu	gtg Val	atg Met	ctc Leu 320	960
gac Asp	gaa Glu	ccg Pro	caa Gln 325	tac Tyr	tgg Trp	aaa Lys	aaa Lys	tat Tyr 330	tat Tyr	cgt Arg	acg Thr	ggt Gly	ttt Phe 335	aac Asn	gat Asp	1008
tca Ser	tta Leu	ctg Leu	gat Asp 340	att Ile	cgt Arg	tac Tyr	agc Ser	ctg Leu 345	tcg Ser	gat Asp	cgt Arg	att Ile	cgt Arg 350	tat Tyr	tac Tyr	1056
tgg Trp	ccg Pro	cat His 355	agt Ser	cgg Arg	att Ile	aaa Lys	aat Asn 360	agc Ser	gtc Val	gaa Glu	acg Thr 365	atg Met	atg Met	gtg Val	aat Asn	1104
ctt Leu	gaa Glu 370	ggc Gly	gtg Val	gac Asp	atc Ile	cca Pro 375	ctg Leu	ggc Gly	atg Met	att Ile	agt Ser 380	cag Gln	tat Tyr	ctt Leu	ccc Pro	1152
aaa Lys 385	caa Gln	ttt Phe	gaa Glu	cgc Arg	att Ile 390	cag Gln	tcc Ser	ggg Gly	gaa Glu	tta Leu 395	tca Ser	gca Ala	ata Ile	ccg Pro	cat His 400	1200

cag	ctg	att	atg	gat	aaa	att	tat	gat	gtt	ttg	cgc	gcc	tat	cgc	tac	1248
Gln	Leu	Ile	Met	Asp	Lys	Ile	Tyr	Asp	Val	Leu	Arg	Ala	Tyr	Arg	Tyr	
				405					410					415		

ggc	tgt	gcg	gaa	taa												1263
Gly	Cys	Ala	Glu	*												
			420													

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 <211> 861
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)...(861)

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Met	Lys	Met	Tyr	Val	Val	Ser	Thr	Lys	Gln	Met	Leu	Asn	Asn	Ala	Gln		
1				5					10					15			
cgc	ggc	ggg	tat	gcg	gtt	ccg	gca	ttc	aat	att	cac	aat	ctc	gaa	acg	96	
Arg	Gly	Gly	Tyr	Ala	Val	Pro	Ala	Phe	Asn	Ile	His	Asn	Leu	Glu	Thr		
			20					25					30				
atg	caa	gtg	gtg	gta	gaa	acc	gct	gcc	aac	ctg	cat	gcg	ccg	gtc	atc	144	
Met	Gln	Val	Val	Val	Glu	Thr	Ala	Ala	Asn	Leu	His	Ala	Pro	Val	Ile		
		35					40					45					
atc	gcc	gga	acg	cct	ggc	aca	ttt	act	cat	gct	ggg	aca	gaa	aat	ctg	192	
Ile	Ala	Gly	Thr	Pro	Gly	Thr	Phe	Thr	His	Ala	Gly	Thr	Glu	Asn	Leu		
		50				55					60						
ttg	gcg	ctg	gtc	agc	gcg	atg	gcg	aag	caa	tat	cac	cat	cca	ctg	gca	240	
Leu	Ala	Leu	Val	Ser	Ala	Met	Ala	Lys	Gln	Tyr	His	His	Pro	Leu	Ala		
65					70					75				80			
att	cat	ctc	gac	cat	cac	acg	aaa	ttt	gac	gat	atc	gct	cag	aag	gtt	288	
Ile	His	Leu	Asp	His	His	Thr	Lys	Phe	Asp	Asp	Ile	Ala	Gln	Lys	Val		
				85					90					95			
cgt	tct	ggc	gtg	cgc	tca	gtc	atg	att	gac	gcc	tcg	cat	ttg	cct	ttt	336	
Arg	Ser	Gly	Val	Arg	Ser	Val	Met	Ile	Asp	Ala	Ser	His	Leu	Pro	Phe		
			100					105					110				
gcg	caa	aat	att	tca	cgg	gtc	aaa	gag	gtg	gtg	gat	ttt	tgc	cat	cgc	384	
Ala	Gln	Asn	Ile	Ser	Arg	Val	Lys	Glu	Val	Val	Asp	Phe	Cys	His	Arg		
		115					120					125					
ttt	gat	gtc	agc	gtc	gag	gcg	gag	ctg	ggg	caa	ctt	ggc	ggc	cag	gaa	432	
Phe	Asp	Val	Ser	Val	Glu	Ala	Glu	Leu	Gly	Gln	Leu	Gly	Gly	Gln	Glu		
		130				135					140						
gat	gat	gtg	caa	gtc	aat	gaa	gcc	gat	gcg	ttg	tac	acc	aac	ccc	gct	480	
Asp	Asp	Val	Gln	Val	Asn	Glu	Ala	Asp	Ala	Leu	Tyr	Thr	Asn	Pro	Ala		

145			150						155						160			
cag	gcg	cgt	gaa	ttt	gcc	gag	gca	acc	gga	att	gat	tcc	ctg	gcg	gtc	528		
Gln	Ala	Arg	Glu	Phe	Ala	Glu	Ala	Thr	Gly	Ile	Asp	Ser	Leu	Ala	Val			
				165			170			175								
gcc	atc	ggc	acg	gct	cat	ggg	atg	tat	gcc	agc	gca	ccg	gcg	ctt	gat	576		
Ala	Ile	Gly	Thr	Ala	His	Gly	Met	Tyr	Ala	Ser	Ala	Pro	Ala	Leu	Asp			
				180			185			190								
ttt	tct	aga	ctg	gag	aac	att	cgc	cag	tgg	gtg	aac	tta	ccg	ctg	gtg	624		
Phe	Ser	Arg	Leu	Glu	Asn	Ile	Arg	Gln	Trp	Val	Asn	Leu	Pro	Leu	Val			
				195			200			205								
ctg	cat	ggc	gcg	tca	ggg	tta	tcg	act	aag	gat	att	cag	caa	acc	atc	672		
Leu	His	Gly	Ala	Ser	Gly	Leu	Ser	Thr	Lys	Asp	Ile	Gln	Gln	Thr	Ile			
				210			215			220								
aaa	ctg	ggg	ata	tgc	aaa	atc	aac	gtt	gca	acg	gag	ctg	aaa	aat	gcc	720		
Lys	Leu	Gly	Ile	Cys	Lys	Ile	Asn	Val	Ala	Thr	Glu	Leu	Lys	Asn	Ala			
				225			230			235			240					
ttc	tcg	cag	gcg	tta	aaa	aat	tac	ctg	acc	gag	cac	cct	gaa	gcg	acc	768		
Phe	Ser	Gln	Ala	Leu	Lys	Asn	Tyr	Leu	Thr	Glu	His	Pro	Glu	Ala	Thr			
				245			250			255								
gat	ccc	cgg	gat	tat	ttg	cag	tcg	gct	aaa	tcc	gca	atg	cgc	gat	gtg	816		
Asp	Pro	Arg	Asp	Tyr	Leu	Gln	Ser	Ala	Lys	Ser	Ala	Met	Arg	Asp	Val			
				260			265			270								
gtg	agc	aaa	gtg	att	gcc	gat	tgt	ggc	tgc	gag	ggc	agg	gca	taa		861		
Val	Ser	Lys	Val	Ile	Ala	Asp	Cys	Gly	Cys	Glu	Gly	Arg	Ala	*				
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<210> 234
<211> 474
<212> DNA
<213> Escherichia coli
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<221> CDS  
<222> (1) ... (474)
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Met	Ser	Gln	Asn	Asp	Ile	Ile	Ile	Arg	Thr	His	Tyr	Lys	Ser	Pro	His	
1				5					10					15		
aga ttg cac atc gat agc gac ata cca aca cct tca tca gag cct att																96
Arg	Leu	His	Ile	Asp	Ser	Asp	Ile	Pro	Thr	Pro	Ser	Ser	Glu	Pro	Ile	
			20					25					30			
aat caa ttt gcg cgc cag ctc atc acc cta ctt gat acc tct gac tta																144
Asn	Gln	Phe	Ala	Arg	Gln	Leu	Ile	Thr	Leu	Leu	Asp	Thr	Ser	Asp	Leu	
		35					40					45				


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<400> 236
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Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15

aac ctc agc gcg aca aac cca ccc gct att ccg cac tgg tgg aag cgt 96
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30

caa ccg ctt att ccc aac ctt ctg tca cag gaa ctg aaa aac tat ctg 144
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45

aag ctt aat gtt aaa gag aaa aat att cag att gca gac cag gta att 192
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60

att gat gaa act gca ggt gaa gtt gtt atc ggc gcg aat acc cgt att 240
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80

tgt cat ggt gcc gtt att cag ggt ccg gta gtg att ggc gca aac tgc 288
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95

ctg ata ggt aat tgg att tgc ccc tat att tcc aga cat ctg tta tca 336
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110

ctt aac cca tta caa gcc cgc tgc cgc aga tat tcc cgt ggc gag cga 384
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

taa 387
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<210> 237
<211> 1197
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(1197)
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<400> 237
atg aaa acc tgg ata ttt atc tgt atg tcc ata gca atg ttg cta tgg 48
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15

ttt tta agt acg cta aga cgt aaa ccc agt caa aag aaa ggc tgt att 96
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30

gac gcc att ata cct gcg tat aac gaa ggc ccg tgt ctg gcg cag tca 144
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Asp	Ala	Ile	Ile	Pro	Ala	Tyr	Asn	Glu	Gly	Pro	Cys	Leu	Ala	Gln	Ser		
	35						40					45					
ctg	gat	aat	cta	ctg	cgt	aac	cct	tat	ttt	tgc	cgg	gta	att	tgc	gtt	192	
Leu	Asp	Asn	Leu	Leu	Arg	Asn	Pro	Tyr	Phe	Cys	Arg	Val	Ile	Cys	Val		
	50					55				60							
aac	gac	ggc	tcc	acg	gac	aat	acc	gaa	gcg	gtc	atg	gcg	gaa	gtc	aaa	240	
Asn	Asp	Gly	Ser	Thr	Asp	Asn	Thr	Glu	Ala	Val	Met	Ala	Glu	Val	Lys		
	65				70				75						80		
cgc	aaa	tgg	ggc	gac	cgc	ttt	gtt	gcc	gtc	acg	caa	aaa	aat	acc	ggc	288	
Arg	Lys	Trp	Gly	Asp	Arg	Phe	Val	Ala	Val	Thr	Gln	Lys	Asn	Thr	Gly		
				85					90					95			
aaa	ggc	ggc	gac	ctg	atg	aat	ggc	ctc	aat	tac	gcc	acc	tgc	gac	cag	336	
Lys	Gly	Gly	Ala	Leu	Met	Asn	Gly	Leu	Asn	Tyr	Ala	Thr	Cys	Asp	Gln		
			100					105					110				
gtt	ttt	tta	agt	gat	gcc	gac	acc	tat	gtt	ccg	ccc	gat	caa	gac	gga	384	
Val	Phe	Leu	Ser	Asp	Ala	Asp	Thr	Tyr	Val	Pro	Pro	Asp	Gln	Asp	Gly		
		115					120					125					
atg	ggc	tat	atg	ctg	gca	gaa	att	gag	cgc	ggc	gcc	gat	gcc	gta	ggc	432	
Met	Gly	Tyr	Met	Leu	Ala	Glu	Ile	Glu	Arg	Gly	Ala	Asp	Ala	Val	Gly		
	130					135					140						
ggc	att	ccc	tct	act	gag	ttg	aaa	ggc	gag	ggc	ctg	tta	ccg	cac	atc	480	
Gly	Ile	Pro	Ser	Thr	Ala	Leu	Lys	Gly	Ala	Gly	Leu	Leu	Pro	His	Ile		
	145				150					155					160		
cgc	gag	acc	gta	aag	ttg	ccg	atg	att	gtt	atg	aag	cgc	acg	cta	cag	528	
Arg	Ala	Thr	Val	Lys	Leu	Pro	Met	Ile	Val	Met	Lys	Arg	Thr	Leu	Gln		
				165					170					175			
cag	ctc	ctg	ggc	ggc	gca	ccg	ttt	att	atc	agc	ggc	gcc	tgc	ggg	atg	576	
Gln	Leu	Leu	Gly	Gly	Ala	Pro	Phe	Ile	Ile	Ser	Gly	Ala	Cys	Gly	Met		
			180					185					190				
ttc	cgt	act	gat	gta	ttg	cgt	aag	ttc	ggc	ttc	tcg	gat	cgt	act	aaa	624	
Phe	Arg	Thr	Asp	Val	Leu	Arg	Lys	Phe	Gly	Phe	Ser	Asp	Arg	Thr	Lys		
		195					200					205					
gtc	gaa	gac	ctt	gat	ctc	acc	tgg	aca	ttg	gtg	gca	aac	ggc	tac	cgt	672	
Val	Glu	Asp	Leu	Asp	Leu	Thr	Trp	Thr	Leu	Val	Ala	Asn	Gly	Tyr	Arg		
	210					215					220						
att	cgg	cag	gag	aat	cgc	tgc	atc	gta	tac	cca	cag	gaa	tgc	aac	agc	720	
Ile	Arg	Gln	Ala	Asn	Arg	Cys	Ile	Val	Tyr	Pro	Gln	Glu	Cys	Asn	Ser		
	225				230					235					240		
ccg	cgt	gag	gag	tgg	cgt	cgc	tgg	cgg	cgt	tgg	att	gtg	gga	tac	gag	768	
Pro	Arg	Glu	Glu	Trp	Arg	Arg	Trp	Arg	Arg	Trp	Ile	Val	Gly	Tyr	Ala		
				245				250						255			
gtc	tgt	atg	cgc	ctg	cat	aaa	aga	ctt	tta	ttt	agc	cgc	ttc	ggc	atc	816	
Val	Cys	Met	Arg	Leu	His	Lys	Arg	Leu	Leu	Phe	Ser	Arg	Phe	Gly	Ile		

260

265

270

ttc agt ata ttt cct atg ctg ttg gtt gtg ctt tat ggc gtt ggg att 864
 Phe Ser Ile Phe Pro Met Leu Leu Val Val Leu Tyr Gly Val Gly Ile
 275 280 285

tat ctc act acc tgg ttt aat gaa ttc atc acc acc ggg ccg cat gga 912
 Tyr Leu Thr Thr Trp Phe Asn Glu Phe Ile Thr Thr Gly Pro His Gly
 290 295 300

gtg gtg ttg gca atg ttt ccg ctt atc tgg gtc ggc gta gtt tgt gtt 960
 Val Val Leu Ala Met Phe Pro Leu Ile Trp Val Gly Val Val Cys Val
 305 310 315 320

att ggt gct ttt agc gcc tgg ttt cat cgt tgc tgg ttg ttg gtg cct 1008
 Ile Gly Ala Phe Ser Ala Trp Phe His Arg Cys Trp Leu Leu Val Pro
 325 330 335

tta gcg ccg ctt tcc gtt gtg tat gta tta tta gct tat gcc atc tgg 1056
 Leu Ala Pro Leu Ser Val Val Tyr Val Leu Leu Ala Tyr Ala Ile Trp
 340 345 350

att att tat gga ctt att gcc ttt ttt act gga cgc gaa cct cag cgc 1104
 Ile Ile Tyr Gly Leu Ile Ala Phe Phe Thr Gly Arg Glu Pro Gln Arg
 355 360 365

gac aaa ccc acc cgc tat tcc gca ctg gtg gaa gcg tca acc gct tat 1152
 Asp Lys Pro Thr Arg Tyr Ser Ala Leu Val Glu Ala Ser Thr Ala Tyr
 370 375 380

tcc caa cct tct gtc aca gga act gaa aaa cta tct gaa gct taa 1197
 Ser Gln Pro Ser Val Thr Gly Thr Glu Lys Leu Ser Glu Ala *
 385 390 395

<210> 238

<211> 1659

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1659)

<400> 238

atg att ctt gag cgc gtt gaa att gtg ggt ttt cgc ggt atc aac cgt 48
 Met Ile Leu Glu Arg Val Glu Ile Val Gly Phe Arg Gly Ile Asn Arg
 1 5 10 15

ttg tcg ttg atg ctg gaa caa aac aac gtc ctg att ggg gag aac gcg 96
 Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala
 20 25 30

tgg ggt aaa tcc agc ttg ctg gac gcc tta act ctg ctg cta tcg cca 144
 Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Ser Pro
 35 40 45

Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser	
500 505 510	
aaa ccc gat ctt gcc att gaa gtg gca atg gag gca gga cgt cgt ggt	1584
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly	
515 520 525	
gtg gac tcc gta ccg acg ctg ctg aaa aaa atg ttc tca cgc gtg ctg	1632
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu	
530 535 540	
tgg ctg gcg cgc ggt cgc gcg gat taa	1659
Trp Leu Ala Arg Gly Arg Ala Asp *	
545 550	

<210> 239
 <211> 1059
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1059)

<400> 239	
atg cta cca tct att tca atc aac aat acc agc gca gct tac cca gaa	48
Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu	
1 5 10 15	
tcc atc aat gaa aat aac aat gat gaa gtt aat gga tta gta caa gag	96
Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu	
20 25 30	
ttc aaa aac ctt ttt aat ggt aag gaa gga ata agc acc tgt att aaa	144
Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys	
35 40 45	
cat cta ctt gag ctt ata aaa aac gcc ata cga gta aac gac gat cct	192
His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro	
50 55 60	
tat aga ttt aat att aat aat tcc tca gtt act tat att gat att gac	240
Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp	
65 70 75 80	
tcc aat gat aca gac cat att act att ggt atc gac aac caa gaa cca	288
Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro	
85 90 95	
ata gaa tta cct gcg aac tat aaa gac aaa gaa ctc gtc cgt act atc	336
Ile Glu Leu Pro Ala Asn Tyr Lys Asp Lys Glu Leu Val Arg Thr Ile	
100 105 110	
att aat gac aac ata gtt gag aag act cat gat atc aat aac aag gaa	384
Ile Asn Asp Asn Ile Val Glu Lys Thr His Asp Ile Asn Asn Lys Glu	
115 120 125	

taa
*

1059

<210> 240
<211> 1128
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1128)

<400> 240
atg atg cgc cat tta cgc aat att ttt aat ctg ggt atc aaa gag ttg 48
Met Met Arg His Leu Arg Asn Ile Phe Asn Leu Gly Ile Lys Glu Leu
1 5 10 15

cgc agt ctg ctc ggt gat aaa gcg atg ctg acg ctg att gtc ttc tcg 96
Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser
20 25 30

ttt acg gtg tcg gtg tat tcg tca gcg acc gtt acg cca gga tcg ttg 144
Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu
35 40 45

aac ctc gcg ccg atc gcc att gcc gat atg gat caa tcg cag tta tcg 192
Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser
50 55 60

aac cgg atc gtt aac agc ttc tat cgt ccg tgg ttt ttg cca ccg gag 240
Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu
65 70 75 80

atg atc acc gcc gat gag atg gat gcc gga ctg gac gcc gga cgc tat 288
Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr
85 90 95

acc ttc gcg ata aat att ccg cct aat ttt cag cgt gat gtc ctc gcc 336
Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala
100 105 110

gga cgc cag ccg gat att cag gtg aac gtc gat gcc acg cgc atg agc 384
Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser
115 120 125

cag gca ttt acc ggc aat ggg tat atc cag aat att atc aac ggt gaa 432
Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu
130 135 140

gtg aac agc ttt gtc gcg cgc tac cgt gat aac agc gaa ccg ttg gta 480
Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val
145 150 155 160

tcg ctg gaa acc cgg atg cgc ttt aac ccg aac ctc gat ccc gcg tgg 528
Ser Leu Glu Thr Arg Met Arg Phe Asn Pro Asn Leu Asp Pro Ala Trp

165										170					175					
ttt	ggc	ggg	gtg	atg	gcg	atc	atc	aac	aac	att	acc	atg	ctg	gcg	att	576				
Phe	Gly	Gly	Val	Met	Ala	Ile	Ile	Asn	Asn	Ile	Thr	Met	Leu	Ala	Ile					
180										185					190					
gta	ttg	acc	gga	tcg	gcg	ctg	atc	cgc	gag	cgt	gaa	cac	ggc	acg	gtg	624				
Val	Leu	Thr	Gly	Ser	Ala	Leu	Ile	Arg	Glu	Arg	Glu	His	Gly	Thr	Val					
195										200					205					
gaa	cac	tta	ctg	gtg	atg	ccg	ata	acg	ccg	ttt	gag	atc	atg	atg	gcg	672				
Glu	His	Leu	Leu	Val	Met	Pro	Ile	Thr	Pro	Phe	Glu	Ile	Met	Met	Ala					
210										215					220					
aag	atc	tgg	tcg	atg	ggg	ctg	gtg	gtg	ctg	gtg	gta	tcg	gga	tta	tcg	720				
Lys	Ile	Trp	Ser	Met	Gly	Leu	Val	Val	Leu	Val	Val	Ser	Gly	Leu	Ser					
225										230					235					
ctg	gtg	ctg	atg	gtg	aaa	ggg	gta	ctg	ggc	gta	ccg	att	gaa	ggc	tcg	768				
Leu	Val	Leu	Met	Val	Lys	Gly	Val	Leu	Gly	Val	Pro	Ile	Glu	Gly	Ser					
245										250					255					
atc	ccg	ctg	ttt	atg	ctg	ggc	gtg	gcg	ctc	agt	ctg	ttt	gcc	acc	acg	816				
Ile	Pro	Leu	Phe	Met	Leu	Gly	Val	Ala	Leu	Ser	Leu	Phe	Ala	Thr	Thr					
260										265					270					
tca	atc	ggc	att	ttt	atg	ggg	acg	ata	gcg	cgt	tca	atg	ccg	caa	ctg	864				
Ser	Ile	Gly	Ile	Phe	Met	Gly	Thr	Ile	Ala	Arg	Ser	Met	Pro	Gln	Leu					
275										280					285					
ggg	ctg	ctg	gtg	att	ctg	gtg	ctg	ctg	ccg	ctg	caa	atg	ctt	tcc	ggt	912				
Gly	Leu	Leu	Val	Ile	Leu	Val	Leu	Leu	Pro	Leu	Gln	Met	Leu	Ser	Gly					
290										295					300					
ggt	tcc	acg	ccg	cgc	gaa	agt	atg	ccg	cag	atg	gtg	cag	gac	att	atg	960				
Gly	Ser	Thr	Pro	Arg	Glu	Ser	Met	Pro	Gln	Met	Val	Gln	Asp	Ile	Met					
305										310					315					
ctg	acc	atg	ccg	acg	aca	cac	ttt	gtt	agc	ctc	gcg	cag	gcc	atc	ctc	1008				
Leu	Thr	Met	Pro	Thr	Thr	His	Phe	Val	Ser	Leu	Ala	Gln	Ala	Ile	Leu					
325										330					335					
tac	cgg	ggt	gcc	gga	ttc	gaa	atc	gtc	tgg	ccg	cag	ttt	ctg	acg	ctg	1056				
Tyr	Arg	Gly	Ala	Gly	Phe	Glu	Ile	Val	Trp	Pro	Gln	Phe	Leu	Thr	Leu					
340										345					350					
atg	gca	att	ggc	ggc	gca	ttt	ttc	acc	att	gcg	ctg	ctg	cga	ttc	agg	1104				
Met	Ala	Ile	Gly	Gly	Ala	Phe	Phe	Thr	Ile	Ala	Leu	Leu	Arg	Phe	Arg					
355										360					365					
aag	acg	att	ggg	aca	atg	gcg	taa									1128				
Lys	Thr	Ile	Gly	Thr	Met	Ala	*													
370										375										

259

<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(2685)

<400> 241

gtg agc cag cat tat gga aaa acc gtt gcg ctg aac aat atc act ctc	48
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1 5 10 15	
gat att ccg gcc cgc tgt atg gtc ggg ctg att ggc ccg gac ggc gtc	96
Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val	
20 25 30	
ggg aag tcg agc ttg ttg tcg ttg att tcc ggt gcc cgc gtc att gaa	144
Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu	
35 40 45	
cag ggc aat gtg atg gtg ctg ggc ggc gat atg cgc gac ccg aag cat	192
Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His	
50 55 60	
cgc cgc gac gtc tgc ccg cgc atc gcc tgg atg ccg cag ggg ctg ggc	240
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly	
65 70 75 80	
aaa aac ctc tac cac acc ttg tcg gtg tat gaa aac gtc gat ttt ttc	288
Lys Asn Leu Tyr His Thr Leu Ser Val Tyr Glu Asn Val Asp Phe Phe	
85 90 95	
gct cgc ctg ttc ggt cac gac aaa gcg gag cgg gaa gtg cga atc aat	336
Ala Arg Leu Phe Gly His Asp Lys Ala Glu Arg Glu Val Arg Ile Asn	
100 105 110	
gag ctg ctg acc agc acc ggg tta gca ccg ttt cgc gat cgt ccg gca	384
Glu Leu Leu Thr Ser Thr Gly Leu Ala Pro Phe Arg Asp Arg Pro Ala	
115 120 125	
ggg aaa ctc tcc ggc ggg atg aag caa aaa ctt ggg ctg tgc tgc gcg	432
Gly Lys Leu Ser Gly Gly Met Lys Gln Lys Leu Gly Leu Cys Cys Ala	
130 135 140	
tta atc cac gac ccg gaa ctg ttg atc ctt gat gag cca aca acg ggg	480
Leu Ile His Asp Pro Glu Leu Leu Ile Leu Asp Glu Pro Thr Thr Gly	
145 150 155 160	
gtt gac ccg ctc tcc cgc tcc cag ttc tgg gat ctg atc gac agt att	528
Val Asp Pro Leu Ser Arg Ser Gln Phe Trp Asp Leu Ile Asp Ser Ile	
165 170 175	
cgc cag cgg cag agc aat atg agc gtg ctg gtc gcc acc gcc tat atg	576
Arg Gln Arg Gln Ser Asn Met Ser Val Leu Val Ala Thr Ala Tyr Met	
180 185 190	
gaa gag gcc gaa cgc ttc gac tgg ctg gta gcg atg aat gcc gga gaa	624

gtg atg ggc tta agt atc ctg ctg ctg aaa aaa cag gag gga tga 2685
 Val Met Gly Leu Ser Ile Leu Leu Leu Lys Lys Gln Glu Gly *
 885 890

<210> 242
 <211> 1068
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1068)

<400> 242
 atg gat aag agt aag cgc cat ctg gcg tgg tgg gtt gtc ggg tta ctg 48
 Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu
 1 5 10 15
 gcg gtg gcg gct atc gtg gcg tgg tgg ctg ttg cgc ccg gca ggt gtg 96
 Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val
 20 25 30
 ccg gaa ggc ttt gct gtc agt aat ggg cgc att gaa gcg acg gaa gtg 144
 Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val
 35 40 45
 gat att gcc agc aaa att gcc ggg cgt atc gac acc att ctg gtg aaa 192
 Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys
 50 55 60
 gaa ggc aag ttt gtt cgc gaa ggt gaa gtg ctg gcg aag atg gat act 240
 Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr
 65 70 75 80
 cgc gtg ttg cag gaa cag cga ctg gaa gcc atc gcg caa atc aaa gag 288
 Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu
 85 90 95
 gca caa agc gcc gtt gct gcc gcg cag gct ttg ctg gag caa cga caa 336
 Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln
 100 105 110
 agc gaa act cgt gcc gca cag tcg ctg gtt aat caa cgc cag gca gaa 384
 Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu
 115 120 125
 ctg gac tcc gta gca aaa cgt cat acg cgt tcc cgt tca ctg gcc caa 432
 Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln
 130 135 140
 cga ggg gct att tct gcg caa cag ctg gat gac gat cgc gcc gcc gct 480
 Arg Gly Ala Ile Ser Ala Gln Gln Leu Asp Asp Asp Arg Ala Ala Ala
 145 150 155 160
 gag agc gcc cga gct gcg ctg gaa tcg gcg aaa gct cag gta tcg gct 528

<220>
 <221> CDS
 <222> (1)...(708)

<400> 243

atg tac cgt tat ttg tct att gct gcg gtg gta ctg agc gca gca ttt	48
Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe	
1 5 10 15	
tcc ggc ccg gcg ttg gcc gaa ggt atc aat agt ttt tct cag gcg aaa	96
Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys	
20 25 30	
gcc gcg gcg gta aaa gtc cac gct gac gcg ccc ggt acg ttt tat tgc	144
Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys	
35 40 45	
gga tgt aaa att aac tgg cag gcc aaa aaa gcc gtt gtt gat ctg caa	192
Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln	
50 55 60	
tcg tgc ggc tat cag gtg cgc aaa aat gaa aac cgc gcc agc cgc gta	240
Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val	
65 70 75 80	
gag tgg gaa cat gtc gtt ccc gcc tgg cag ttc ggt cac cag cgc cag	288
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln	
85 90 95	
tgc tgg cag gac ggt gga cgt aaa aac tgc gct aaa gat ccg gtc tat	336
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr	
100 105 110	
cgc aag atg gaa agc gat atg cat aac ctg cag ccg tca gtc ggt gag	384
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu	
115 120 125	
gtg aat ggc gat cgc gcc aac ttt atg tac agc cag tgg aat ggc ggt	432
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly	
130 135 140	
gaa ggc cag tac ggt caa tgc gcc atg aag gtc gat ttc aaa gaa aaa	480
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys	
145 150 155 160	
gct gcc gaa cca cca gcg cgt gca cgc ggt gcc att gcg cgc acc tac	528
Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr	
165 170 175	
ttc tat atg cgc gac caa tac aac ctg aca ctc tct cgc cag caa acg	576
Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr	
180 185 190	
cag ctg ttc aac gca tgg aac aag atg tat ccg gtt acc gac tgg gag	624
Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu	
195 200 205	

tgc gag cgc gat gaa cgc atc gcg aag gtg cag ggc aat cat aac ccg 672
 Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
 210 215 220

tat gtg caa cgc gct tgc cag gcg cga aag agc taa 708
 Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser *
 225 230 235

<210> 244
 <211> 1443
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1443)

<400> 244
 atg tcc aga agg ctt cgc aga aca aaa atc gtt acc acg tta ggc cca 48
 Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro
 1 5 10 15

gca aca gat cgc gat aat aat ctt gaa aaa gtt atc gcg gcg ggt gcc 96
 Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala
 20 25 30

aac gtt gta cgt atg aac ttt tct cac ggc tcg cct gaa gat cac aaa 144
 Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys
 35 40 45

atg cgc gcg gat aaa gtt cgt gag att gcc gca aaa ctg ggg cgt cat 192
 Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His
 50 55 60

gtg gct att ctg ggt gac ctc cag ggg ccc aaa atc cgt gta tcc acc 240
 Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr
 65 70 75 80

ttt aaa gaa ggc aaa gtt ttc ctc aat att ggg gat aaa ttc ctg ctc 288
 Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu
 85 90 95

gac gcc aac ctg ggt aaa ggt gaa ggc gac aaa gaa aaa gtc ggt atc 336
 Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile
 100 105 110

gac tac aaa ggc ctg cct gct gac gtc gtg cct ggt gac atc ctg ctg 384
 Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu
 115 120 125

ctg gac gat ggt cgc gtc cag tta aaa gta ctg gaa gtt cag ggc atg 432
 Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met
 130 135 140

aaa gtg ttc acc gaa gtc acc gtc ggt ggt ccc ctc tcc aac aat aaa 480
 Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys

145	150	155	160	
ggt atc aac aaa ctt ggc ggc ggt ttg tgc gct gaa gcg ctg acc gaa				528
Gly Ile Asn Lys Leu Gly Gly Gly Leu Ser Ala Glu Ala Leu Thr Glu				
	165	170	175	
aaa gac aaa gca gac att aag act gcg gcg ttg att ggc gta gat tac				576
Lys Asp Lys Ala Asp Ile Lys Thr Ala Ala Leu Ile Gly Val Asp Tyr				
	180	185	190	
ctg gct gtc tcc ttc cca cgc tgt ggc gaa gat ctg aac tat gcc cgt				624
Leu Ala Val Ser Phe Pro Arg Cys Gly Glu Asp Leu Asn Tyr Ala Arg				
	195	200	205	
cgc ctg gca cgc gat gca gga tgt gat gcg aaa att gtt gcc aag gtt				672
Arg Leu Ala Arg Asp Ala Gly Cys Asp Ala Lys Ile Val Ala Lys Val				
	210	215	220	
gaa cgt gcg gaa gcc gtt tgc agc cag gat gca atg gat gac atc atc				720
Glu Arg Ala Glu Ala Val Cys Ser Gln Asp Ala Met Asp Asp Ile Ile				
	225	230	235	240
ctc gcc tct gac gtg gta atg gtt gca cgt ggc gac ctc ggt gtg gaa				768
Leu Ala Ser Asp Val Val Met Val Ala Arg Gly Asp Leu Gly Val Glu				
	245	250	255	
att ggc gac ccg gaa ctg gtc ggc att cag aaa gcg ttg atc cgt cgt				816
Ile Gly Asp Pro Glu Leu Val Gly Ile Gln Lys Ala Leu Ile Arg Arg				
	260	265	270	
gcg cgt cag cta aac cga gcg gta atc acg gcg acc cag atg atg gag				864
Ala Arg Gln Leu Asn Arg Ala Val Ile Thr Ala Thr Gln Met Met Glu				
	275	280	285	
tca atg att act aac ccg atg ccg acg cgt gca gaa gtc atg gac gta				912
Ser Met Ile Thr Asn Pro Met Pro Thr Arg Ala Glu Val Met Asp Val				
	290	295	300	
gca aac gcc gtt ctg gat ggt act gac gct gtg atg ctg tct gca gaa				960
Ala Asn Ala Val Leu Asp Gly Thr Asp Ala Val Met Leu Ser Ala Glu				
	305	310	315	320
act gcc gct ggg cag tat ccg tca gaa acc gtt gca gcc atg gcg cgc				1008
Thr Ala Ala Gly Gln Tyr Pro Ser Glu Thr Val Ala Ala Met Ala Arg				
	325	330	335	
gtt tgc ctg ggt gcg gaa aaa atc ccg agc atc aac gtt tct aaa cac				1056
Val Cys Leu Gly Ala Glu Lys Ile Pro Ser Ile Asn Val Ser Lys His				
	340	345	350	
cgt ctg gac gtt cag ttc gac aat gtg gaa gaa gct att gcc atg tca				1104
Arg Leu Asp Val Gln Phe Asp Asn Val Glu Glu Ala Ile Ala Met Ser				
	355	360	365	
gca atg tac gca gct aac cac ctg aaa ggc gtt acg gcg atc atc acc				1152
Ala Met Tyr Ala Ala Asn His Leu Lys Gly Val Thr Ala Ile Ile Thr				
	370	375	380	

atg acc gaa tcg ggt cgt acc gcg ctg atg acc tcc cgt atc agc tct	1200
Met Thr Glu Ser Gly Arg Thr Ala Leu Met Thr Ser Arg Ile Ser Ser	
385 390 395 400	

ggc ctg cca att ttc gcc atg tcg cgc cat gaa cgt acg ctg aac ctg	1248
Gly Leu Pro Ile Phe Ala Met Ser Arg His Glu Arg Thr Leu Asn Leu	
405 410 415	

act gct ctc tat cgt ggc gtt acg ccg gtg cac ttt gat agc gct aat	1296
Thr Ala Leu Tyr Arg Gly Val Thr Pro Val His Phe Asp Ser Ala Asn	
420 425 430	

gac ggc gta gca gct gcc agc gaa gcg gtt aat ctg ctg cgc gat aaa	1344
Asp Gly Val Ala Ala Ala Ser Glu Ala Val Asn Leu Leu Arg Asp Lys	
435 440 445	

ggc tac ttg atg tct ggt gac ctg gtg att gtc acc cag ggc gac gtg	1392
Gly Tyr Leu Met Ser Gly Asp Leu Val Ile Val Thr Gln Gly Asp Val	
450 455 460	

atg agt acc gtg ggt tct act aat acc acg cgt att tta acg gta gag	1440
Met Ser Thr Val Gly Ser Thr Asn Thr Thr Arg Ile Leu Thr Val Glu	
465 470 475 480	

taa	1443
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<210> 245
 <211> 720
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(720)

<400> 245	
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Met Ile Asn Val Leu Ile Ile Asp Asp Ala Met Val Ala Glu Leu	
1 5 10 15	

aat cgc cga tac gta gca caa atc cca ggc ttt caa tgc tgt gga aca	96
Asn Arg Arg Tyr Val Ala Gln Ile Pro Gly Phe Gln Cys Cys Gly Thr	
20 25 30	

gcc tcg acg ctg gag aaa gcc aaa gag att atc ttc aat agc gat acg	144
Ala Ser Thr Leu Glu Lys Ala Lys Glu Ile Ile Phe Asn Ser Asp Thr	
35 40 45	

cct atc gac ctg ata ttg ctc gat atc tat atg caa aaa gag aac ggg	192
Pro Ile Asp Leu Ile Leu Leu Asp Ile Tyr Met Gln Lys Glu Asn Gly	
50 55 60	

ctc gat tta ctg cct gtc ctg cat aac gcg cgt tgc aaa agt gat gtg	240
---	-----

1	5	10	15	
ttg agt acc aca gtg atc tta atg gtc agt gcg gta ctg ttc tcg gtg				96
Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val	20	25	30	
cta ttg gtg gtg cat ctg att tac ttc tcg caa atc agt gat atg acg				144
Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr	35	40	45	
cga gat ggg cta gcc aac aag gca ctg gca gtg gcg cgt acc ctc gcc				192
Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala	50	55	60	
gac tcg ccg gaa atc cgt cag gcc ttg cag aaa aaa ccg cag gag agt				240
Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser	65	70	75	80
ggc atc cag gcc atc gcg gaa gcc gta cgc aaa cgc aac gat ctg ctg				288
Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu	85	90	95	
ttt att gtc gtt acc gat atg caa agt ctt cgc tac tcg cat cct gaa				336
Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu	100	105	110	
gcc cag cgt att ggt cag cca ttt aaa ggt gat gac atc ctt aaa gcg				384
Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala	115	120	125	
ctg aat ggc gaa gaa aat gtc gct atc aat cgc ggt ttt ctg gcg cag				432
Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln	130	135	140	
gct tta cgc gta ttt acc ccc atc tac gat gaa aat cat aaa caa att				480
Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile	145	150	155	160
ggc gtg gtg gcg atc ggc ctt gag tta agc cgt gtg acc caa cag atc				528
Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile	165	170	175	
aat gac agt cgc tgg agc att atc tgg tcg gta tta ttt ggc atg ctg				576
Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu	180	185	190	
gtc gga ctg att ggc acc tgc att ctg gtt aag gta ctg aaa aaa atc				624
Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile	195	200	205	
ctt ttc ggc ctg gaa ccc tac gaa atc tcc acg ctg ttt gag caa cgc				672
Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg	210	215	220	
cag gcc atg ttg cag tct atc aaa gaa ggc gtc gtt gcc gtg gac gat				720
Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp	225	230	235	240

cgt cac ggc tgg ctg cac tgt gaa gtt aat gat gat gga ccg ggg atc	1440
Arg His Gly Trp Leu His Cys Glu Val Asn Asp Asp Gly Pro Gly Ile	
465 470 475 480	
gca ccc gat aaa atc gat cac att ttt gac aaa ggt gtc tcg aca aaa	1488
Ala Pro Asp Lys Ile Asp His Ile Phe Asp Lys Gly Val Ser Thr Lys	
485 490 495	
gga agc gag cga ggc gtc ggt tta gca ctt gtc aaa caa cag gta gaa	1536
Gly Ser Glu Arg Gly Val Gly Leu Ala Leu Val Lys Gln Gln Val Glu	
500 505 510	
aat ctc ggc ggc agc atc gcc gtg gaa tcg gaa ccc ggg att ttc aca	1584
Asn Leu Gly Gly Ser Ile Ala Val Glu Ser Glu Pro Gly Ile Phe Thr	
515 520 525	
caa ttt ttt gtc cag ata ccc tgg gac ggg gag agg tcg aac aga tga	1632
Gln Phe Phe Val Gln Ile Pro Trp Asp Gly Glu Arg Ser Asn Arg *	
530 535 540	

<210> 247
 <211> 987
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(987)

<400> 247	
ttg agt gta ccg ctg tcg aca tgg aat ctt ctg cga tac aac aat tcg	48
Met Ser Val Pro Leu Ser Thr Trp Asn Leu Leu Arg Tyr Asn Asn Ser	
1 5 10 15	
tat cta cag aag gta act atg ttt cca caa tgc aaa ttt tcc cgc gag	96
Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu	
20 25 30	
ttt cta cat cct cgc tac tgg ctc aca tgg ttt ggg ctt ggt gta ctc	144
Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu	
35 40 45	
tgg ctt tgg gta cag ctt cct tat cct gtt ctc tgc ttt ctc ggc acg	192
Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr	
50 55 60	
cgt att ggc gca atg gcg cga cca ttc ctg aaa cgt cgt gaa tct atc	240
Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile	
65 70 75 80	
gcc cgt aaa aac ctg gaa ctt tgt ttc ccg cag cat tct gcg gaa gaa	288
Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu	
85 90 95	
cgc gag aag atg att gcc gaa aac ttt cgt tca ctc ggc atg gcg ctg	336

Arg	Glu	Lys	Met 100	Ile	Ala	Glu	Asn	Phe	Arg	Ser	Leu	Gly	Met 110	Ala	Leu	
gta	gaa	acc	ggc	atg	gca	tgg	ttc	tgg	ccc	gac	agt	cgc	gta	cgt	aaa	384
Val	Glu	Thr	Gly	Met	Ala	Trp	Phe	Trp	Pro	Asp	Ser	Arg	Val	Arg	Lys	
			115				120					125				
tgg	ttt	gat	gtt	gaa	ggg	ttg	gat	aac	ctt	aaa	cgc	gca	caa	atg	caa	432
Trp	Phe	Asp	Val	Glu	Gly	Leu	Asp	Asn	Leu	Lys	Arg	Ala	Gln	Met	Gln	
			130				135				140					
aat	cgc	ggc	gta	atg	gtt	gtc	ggc	gtc	cat	ttt	atg	tcg	ctg	gaa	ctg	480
Asn	Arg	Gly	Val	Met	Val	Val	Gly	Val	His	Phe	Met	Ser	Leu	Glu	Leu	
145					150					155					160	
ggc	ggc	cgc	gtg	atg	gga	ctg	tgc	caa	cca	atg	atg	gct	acc	tat	cgt	528
Gly	Gly	Arg	Val	Met	Gly	Leu	Cys	Gln	Pro	Met	Met	Ala	Thr	Tyr	Arg	
				165					170					175		
cca	cat	aat	aat	cag	ctg	atg	gaa	tgg	gtg	cag	acc	cgt	ggg	cgc	atg	576
Pro	His	Asn	Asn	Gln	Leu	Met	Glu	Trp	Val	Gln	Thr	Arg	Gly	Arg	Met	
			180					185					190			
cgc	tct	aac	aaa	gcg	atg	atc	ggc	aga	aat	aat	ctg	cgc	ggc	att	gtc	624
Arg	Ser	Asn	Lys	Ala	Met	Ile	Gly	Arg	Asn	Asn	Leu	Arg	Gly	Ile	Val	
		195					200					205				
ggc	gca	ctg	aag	aaa	ggc	gaa	gcg	gta	tgg	ttt	gct	ccc	gat	cag	gat	672
Gly	Ala	Leu	Lys	Lys	Gly	Glu	Ala	Val	Trp	Phe	Ala	Pro	Asp	Gln	Asp	
	210					215					220					
tat	ggc	cgt	aaa	ggc	agc	tcc	ttc	gcg	ccg	ttc	ttt	gcg	gtg	gaa	aat	720
Tyr	Gly	Arg	Lys	Gly	Ser	Ser	Phe	Ala	Pro	Phe	Phe	Ala	Val	Glu	Asn	
225					230					235					240	
gtc	gcc	aca	acc	aat	ggc	acc	tat	gtt	ctc	tcc	cgt	ctc	tct	ggc	gca	768
Val	Ala	Thr	Thr	Asn	Gly	Thr	Tyr	Val	Leu	Ser	Arg	Leu	Ser	Gly	Ala	
				245					250					255		
gcc	atg	ttg	acc	gta	acg	atg	gta	aga	aaa	gcg	gat	tac	agc	gga	tat	816
Ala	Met	Leu	Thr	Val	Thr	Met	Val	Arg	Lys	Ala	Asp	Tyr	Ser	Gly	Tyr	
			260					265					270			
cgt	ttg	ttc	atc	acc	cca	gag	atg	gaa	ggc	tac	ccg	aca	gat	gaa	aat	864
Arg	Leu	Phe	Ile	Thr	Pro	Glu	Met	Glu	Gly	Tyr	Pro	Thr	Asp	Glu	Asn	
		275					280					285				
caa	gcc	gct	gcc	tat	atg	aac	aag	att	atc	gag	aaa	gag	atc	atg	cgc	912
Gln	Ala	Ala	Ala	Tyr	Met	Asn	Lys	Ile	Ile	Glu	Lys	Glu	Ile	Met	Arg	
	290					295					300					
gca	ccg	gag	cag	tac	ctc	tgg	atc	cac	cgt	cgc	ttt	aaa	acg	cgc	ccg	960
Ala	Pro	Glu	Gln	Tyr	Leu	Trp	Ile	His	Arg	Arg	Phe	Lys	Thr	Arg	Pro	
305					310											

<210> 248
 <211> 264
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(264)

<400> 248
 ttg gct aat atc aaa tca gct aag aag cgc gcc att cag tct gaa aag 48
 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 gct cgt aag cac aac gca agc cgt cgc tct atg atg cgt act ttc atc 96
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 aag aaa gta tac gca gct atc gaa gct ggc gac aaa gct gct gca cag 144
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 aaa gca ttt aac gaa atg caa ccg atc gtg gac cgt cag gct gct aaa 192
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 ggt ctg atc cac aaa aac aaa gct gca cgt cat aag gct aac ctg act 240
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 gca cag atc aac aaa ctg gct taa 264
 Ala Gln Ile Asn Lys Leu Ala *
 85

<210> 249
 <211> 1293
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1293)

<400> 249
 atg cgc tat aat ggt tta aat aat atg ttt ttc cct ctt tgc ctg att 48
 Met Arg Tyr Asn Gly Leu Asn Asn Met Phe Phe Pro Leu Cys Leu Ile
 1 5 10 15
 aac gat aac cac tct gtc aca agt cca tca cat aca aag aaa aca aaa 96
 Asn Asp Asn His Ser Val Thr Ser Pro Ser His Thr Lys Lys Thr Lys
 20 25 30
 tca gat aat tac agc aaa cat cat aaa aac acg tta att gac aat aaa 144

Ser	Asp	Asn	Tyr	Ser	Lys	His	His	Lys	Asn	Thr	Leu	Ile	Asp	Asn	Lys		
		35					40					45					
gcc	ctc	tct	ctt	ttc	aaa	atg	gat	gat	cat	gaa	aaa	gtg	ata	ggc	ttg	192	
Ala	Leu	Ser	Leu	Phe	Lys	Met	Asp	Asp	His	Glu	Lys	Val	Ile	Gly	Leu		
	50					55					60						
att	cag	aaa	atg	aaa	aga	att	tat	gat	agt	tta	cca	tca	gga	aaa	atc	240	
Ile	Gln	Lys	Met	Lys	Arg	Ile	Tyr	Asp	Ser	Leu	Pro	Ser	Gly	Lys	Ile		
	65				70					75					80		
acg	aaa	gaa	acg	gac	agg	aaa	ata	cat	aaa	tat	ttt	ata	gat	ata	gct	288	
Thr	Lys	Glu	Thr	Asp	Arg	Lys	Ile	His	Lys	Tyr	Phe	Ile	Asp	Ile	Ala		
				85					90					95			
tca	cat	gca	aat	aat	aaa	tgt	gac	gat	aga	att	acg	aga	aga	ggt	tac	336	
Ser	His	Ala	Asn	Asn	Lys	Cys	Asp	Asp	Arg	Ile	Thr	Arg	Arg	Val	Tyr		
			100					105						110			
ctt	aat	aaa	gat	aag	gaa	gtg	tca	att	aag	gtg	gta	tat	ttt	ata	aat	384	
Leu	Asn	Lys	Asp	Lys	Glu	Val	Ser	Ile	Lys	Val	Val	Tyr	Phe	Ile	Asn		
		115					120					125					
aat	gtc	acc	gtc	cat	aat	aat	act	atc	gaa	atc	cca	cag	aca	gta	aat	432	
Asn	Val	Thr	Val	His	Asn	Asn	Thr	Ile	Glu	Ile	Pro	Gln	Thr	Val	Asn		
	130					135					140						
ggt	ggt	tac	gat	ttt	tca	cac	ctt	agc	ctg	aaa	ggt	atc	gtg	att	aaa	480	
Gly	Gly	Tyr	Asp	Phe	Ser	His	Leu	Ser	Leu	Lys	Gly	Ile	Val	Ile	Lys		
	145				150					155					160		
gat	gaa	gat	tta	tcc	aat	tcg	aat	ttt	gca	ggt	tgc	aga	cta	caa	aac	528	
Asp	Glu	Asp	Leu	Ser	Asn	Ser	Asn	Phe	Ala	Gly	Cys	Arg	Leu	Gln	Asn		
				165					170					175			
gct	att	ttt	cag	gac	tgt	aat	atg	tat	aaa	acg	aat	ttt	aat	ttc	gcc	576	
Ala	Ile	Phe	Gln	Asp	Cys	Asn	Met	Tyr	Lys	Thr	Asn	Phe	Asn	Phe	Ala		
			180					185					190				
ata	atg	gaa	aaa	ata	ctt	ttt	gat	aat	tgt	att	ctc	gat	gac	tca	aat	624	
Ile	Met	Glu	Lys	Ile	Leu	Phe	Asp	Asn	Cys	Ile	Leu	Asp	Asp	Ser	Asn		
		195					200					205					
ttc	gct	cag	ata	aaa	atg	act	gac	gga	act	cta	aat	tca	tgt	tcc	gct	672	
Phe	Ala	Gln	Ile	Lys	Met	Thr	Asp	Gly	Thr	Leu	Asn	Ser	Cys	Ser	Ala		
	210					215					220						
atg	cat	gtt	caa	ttc	tac	aat	gca	aca	atg	aat	aga	gcc	aat	att	aaa	720	
Met	His	Val	Gln	Phe	Tyr	Asn	Ala	Thr	Met	Asn	Arg	Ala	Asn	Ile	Lys		
	225				230					235					240		
aat	acc	ttc	ctt	gat	tat	tca	aat	ttt	tat	atg	gca	tac	atg	gct	gag	768	
Asn	Thr	Phe	Leu	Asp	Tyr	Ser	Asn	Phe	Tyr	Met	Ala	Tyr	Met	Ala	Glu		
				245					250					255			
gta	aat	ctt	tat	aaa	gta	ata	gcg	cca	tat	att	aat	tta	ttt	aga	gcc	816	
Val	Asn	Leu	Tyr	Lys	Val	Ile	Ala	Pro	Tyr	Ile	Asn	Leu	Phe	Arg	Ala		

260	265	270	
gac ctt agc ttc tct aaa ctt gat tta att aac ttt gaa cat gct gat			864
Asp Leu Ser Phe Ser Lys Leu Asp Leu Ile Asn Phe Glu His Ala Asp			
275	280	285	
ctg tct cgt gtc aac ctg aat aaa gca acc ctc cag aat ata aac tta			912
Leu Ser Arg Val Asn Leu Asn Lys Ala Thr Leu Gln Asn Ile Asn Leu			
290	295	300	
att gat agc aaa ctc ttt ttt acg cgg tta aca aat acg ttc ctc gaa			960
Ile Asp Ser Lys Leu Phe Phe Thr Arg Leu Thr Asn Thr Phe Leu Glu			
305	310	315	320
atg gtt ata tgt acc gac tct aat atg gct aat gtt aat ttt aat aat			1008
Met Val Ile Cys Thr Asp Ser Asn Met Ala Asn Val Asn Phe Asn Asn			
325	330	335	
gcc aat tta agc aat tgc cat ttc aac tgt tct gtt tta aca aaa gcc			1056
Ala Asn Leu Ser Asn Cys His Phe Asn Cys Ser Val Leu Thr Lys Ala			
340	345	350	
tgg atg ttt aat atc cgt ctc tat cgt gtt aat ttc gat gag gct agc			1104
Trp Met Phe Asn Ile Arg Leu Tyr Arg Val Asn Phe Asp Glu Ala Ser			
355	360	365	
gtc cag gga atg ggt att acc att ctc cgt ggt gag gaa aat atc tcc			1152
Val Gln Gly Met Gly Ile Thr Ile Leu Arg Gly Glu Glu Asn Ile Ser			
370	375	380	
att aat agt gat atc ctg gta aca cta cag aaa ttc ttt gaa gaa gat			1200
Ile Asn Ser Asp Ile Leu Val Thr Leu Gln Lys Phe Phe Glu Glu Asp			
385	390	395	400
tgt gcc act cat act ggc atg tca caa act gag gat aat ctt cat gca			1248
Cys Ala Thr His Thr Gly Met Ser Gln Thr Glu Asp Asn Leu His Ala			
405	410	415	
gtc gct atg aag att act gca gat att atg caa gat gca gat tga			1293
Val Ala Met Lys Ile Thr Ala Asp Ile Met Gln Asp Ala Asp *			
420	425	430	

<210> 250
 <211> 2652
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2652)

<400> 250
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 Met Asn Glu Gln Tyr Ser Ala Leu Arg Ser Asn Val Ser Met Leu Gly
 1 5 10 15

690	695	700	
cca acc ggc ggc gtc	gag tca cta cgc gcc	att ccg tgg atc ttc gcc	2160
Pro Thr Gly Gly Val	Glu Ser Leu Arg Ala	Ile Pro Trp Ile Phe Ala	
705	710	715 720	
tgg acg caa aac cgt	ctg atg ctc ccc gcc	tgg ctg ggt gca ggt acg	2208
Trp Thr Gln Asn Arg	Leu Met Leu Pro Ala	Trp Leu Gly Ala Gly Thr	
	725	730 735	
gcg ctg caa aaa gtg	gtc gaa gac ggc aaa	cag agc gag ctg gag gct	2256
Ala Leu Gln Lys Val	Val Glu Asp Gly Lys	Gln Ser Glu Leu Glu Ala	
	740	745 750	
atg tgc cgc gat tgg	cca ttc ttc tgc acg	cgt ctc ggc atg ctg gag	2304
Met Cys Arg Asp Trp	Pro Phe Phe Ser Thr	Arg Leu Gly Met Leu Glu	
	755	760 765	
atg gtc ttc gcc aaa	gca gac ctg tgg ctg	gcg gaa tac tat gac caa	2352
Met Val Phe Ala Lys	Ala Asp Leu Trp Leu	Ala Glu Tyr Tyr Asp Gln	
	770	775 780	
cgc ctg gta gac aaa	gca ctg tgg ccg tta	ggt aaa gag tta cgc aac	2400
Arg Leu Val Asp Lys	Ala Leu Trp Pro Leu	Gly Lys Glu Leu Arg Asn	
785	790	795 800	
ctg caa gaa gaa gac	atc aaa gtg gtg ctg	gcg att gcc aac gat tcc	2448
Leu Gln Glu Glu Asp	Ile Lys Val Val Leu	Ala Ile Ala Asn Asp Ser	
	805	810 815	
cat ctg atg gcc gat	ctg ccg tgg att gca	gag tct att cag cta cgg	2496
His Leu Met Ala Asp	Leu Pro Trp Ile Ala	Glu Ser Ile Gln Leu Arg	
	820	825 830	
aat att tac acc gac	ccg ctg aac gta ttg	cag gcc gag ttg ctg cac	2544
Asn Ile Tyr Thr Asp	Pro Leu Asn Val Leu	Gln Ala Glu Leu Leu His	
	835	840 845	
cgc tcc cgc cag gca	gaa aaa gaa ggc cag	gaa ccg gat cct cgc gtc	2592
Arg Ser Arg Gln Ala	Glu Lys Glu Gly Gln	Glu Pro Asp Pro Arg Val	
	850	855 860	
gaa caa gcg tta atg	gtc act att gcc ggg	att gcg gca ggt atg cgt	2640
Glu Gln Ala Leu Met	Val Thr Ile Ala Gly	Ile Ala Ala Gly Met Arg	
865	870	875 880	
aat acc ggc taa			2652
Asn Thr Gly *			

<210> 251
 <211> 1992
 <212> DNA
 <213> Escherichia coli
 <220>

<221> CDS
 <222> (1)...(1992)

<400> 251

atg tcc tca cgt aaa gag ctt gcc aat gct att cgt gcg ctg agc atg	48
Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met	
1 5 10 15	
 gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt	96
Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly	
20 25 30	
 atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac	144
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn	
35 40 45	
 ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac	192
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn	
50 55 60	
 ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac	240
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr	
65 70 75 80	
 gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa	288
Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys	
85 90 95	
 act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc	336
Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr	
100 105 110	
 acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att	384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile	
115 120 125	
 gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att	432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile	
130 135 140	
 gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa	480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu	
145 150 155 160	
 ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt	528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly	
165 170 175	
 aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac	576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His	
180 185 190	
 gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac	624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr	
195 200 205	
 ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc	672

435	440	445	
gcg ctg atg aaa cag cgt cag gtg atg gtt tac acc cac gac tcc atc Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile 450 455 460			1392
ggg ctg ggc gaa gac ggg ccg act cac cag ccg gtt gag cag gtc gct Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala 465 470 475 480			1440
tct ctg cgc gta acc ccg aac atg tct aca tgg cgt ccg tgt gac cag Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln 485 490 495			1488
gtt gaa tcc gcg gtc gcg tgg aaa tac ggt gtt gag cgt cag gac ggc Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly 500 505 510			1536
ccg acc gca ctg atc ctc tcc cgt cag aac ctg gcg cag cag gaa cga Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg 515 520 525			1584
act gaa gag caa ctg gca aac atc gcg cgc ggt ggt tat gtg ctg aaa Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys 530 535 540			1632
gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu 545 550 555 560			1680
gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val 565 570 575			1728
aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln 580 585 590			1776
gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg 595 600 605			1824
gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly 610 615 620			1872
ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro 625 630 635 640			1920
gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val 645 650 655			1968
gcg aaa gca aaa gaa ctg ctg taa Ala Lys Ala Lys Glu Leu Leu *			1992
660			

<210> 252
 <211> 459
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(459)

<400> 252
 atg ttc cgg gga gca acg tta gtc aat ctc gac agc aaa ggg cgc tta 48
 Met Phe Arg Gly Ala Thr Leu Val Asn Leu Asp Ser Lys Gly Arg Leu
 1 5 10 15
 tca gtg cct acc cgt tat cgg gaa cag ctg ctt gag aac gct gcc ggt 96
 Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly
 20 25 30
 caa atg gtt tgc acc att gac att tat cac ccg tgc ctg ctg ctt tac 144
 Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Leu Tyr
 35 40 45
 ccc ctg cct gaa tgg gaa att atc gag caa aaa tta tcg cgt ctg tcg 192
 Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser
 50 55 60
 agc atg aac ccg gtt gag cgc cgt gtg cag cgc cta ctg tta ggt cat 240
 Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His
 65 70 75 80
 gcc agc gaa tgt cag atg gat ggc gca ggt cga ttg tta atc gcg cca 288
 Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
 85 90 95
 gta ctg cgg caa cat gcc ggg ctg aca aaa gaa gtg atg ctg gtt gga 336
 Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
 100 105 110
 cag ttc aac aag ttt gag ctg tgg gat gaa aca acc tgg cat caa cag 384
 Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
 115 120 125
 gtc aag gaa gat atc gac gca gag cag ttg gct acc gga gac tta tcg 432
 Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
 130 135 140
 gag cga ctg cag gac ttg tct cta taa 459
 Glu Arg Leu Gln Asp Leu Ser Leu *
 145 150

<210> 253
 <211> 942
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(942)

<400> 253

atg atg gaa aac tat aaa cat act acg gtg ctg ctg gat gaa gcc gtt	48
Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val	
1 5 10 15	
aat ggc ctc aat atc cgt cct gat ggc atc tac att gat ggg act ttt	96
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe	
20 25 30	
ggg cgc ggt ggt cac tca cgt ctg atc ctc tcg cag ctt ggc gaa gag	144
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu	
35 40 45	
ggg cgt ttg ctg gcg atc gat cgc gac ccg cag gct atc gcc gtt gcg	192
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala	
50 55 60	
aag act att gat gat ccg cgc ttc tcc atc atc cac gga cct ttc tcc	240
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser	
65 70 75 80	
gcg ctg ggc gaa tac gtt gcc gag cgc gat ctt atc ggc aag atc gac	288
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp	
85 90 95	
ggc att ctc ctc gat ctt ggc gtc tct tca ccg caa ctt gat gat gct	336
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala	
100 105 110	
gaa cgt ggc ttt tcc ttt atg cgc gat ggt ccg ctg gac atg cgt atg	384
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met	
115 120 125	
gac cca acc cgt ggg cag tca gcc gct gaa tgg cta caa acc gca gaa	432
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu	
130 135 140	
gaa gcc gat atc gcc tgg gta ttg aaa acc tat ggt gaa gag cgt ttt	480
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe	
145 150 155 160	
gcc aaa cgc att gcc cgc gcc att gtc gag cgt aac cgc gaa cag ccg	528
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro	
165 170 175	
atg acc cgc acc aaa gaa ctg gcg gaa gtc gtg gct gct gca acg ccg	576
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro	
180 185 190	
gtg aaa gat aag ttt aaa cat ccc gcg acc cgt acc ttc cag gcg gtg	624
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val	
195 200 205	

cgc att tgg gta aac agt gaa ctg gag gag ata gag cag gcg cta aaa 672
 Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
 210 215 220

agc tcg ctc aac gtg ctg gcc ccg ggt ggg cgg ctt tcg atc atc agc 720
 Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
 225 230 235 240

ttc	cac	tcg	ctg	gaa	gac	cgt	att	gtg	aaa	cgt	ttt	atg	cgt	gaa	aac	768
Phe	His	Ser	Leu	Glu	Asp	Arg	Ile	Val	Lys	Arg	Phe	Met	Arg	Glu	Asn	
				245					250					255		

agc cgc ggt ccg caa gtt ccg gca ggg tta ccg atg act gaa gag cag 816
 Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
 260 265 270

ctc aaa aaa ctg ggt ggc cgt cag ctg cga gca cta ggc aag tta atg 864
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285

ccg ggc gaa gaa gag gtg gct gag aac cct cgt gcc cgt agt tca gtt 912
 Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
 290 295 300

ctg cgt att gca gag agg acg aat gca tga 942
Leu Arg Ile Ala Glu Arg Thr Asn Ala *
305 310

<210> 254

<211> 366

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) ... (366)

<400> 254

atg atc agc aga gtg aca gaa gct cta agc aaa gtt aaa gga tcg atg 48
Met Ile Ser Arg Val Thr Glu Ala Leu Ser Lys Val Lys Gly Ser Met
1 5 10 15

gga agc cac gag cgc cat gca ttg cct ggt gtt atc ggt gac gat ctt 96
Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
20 25 30

ttg	cga	ttt	ggg	aag	ctg	cca	ctc	tgc	ctg	ttc	att	tgc	att	att	ttg	144
Leu	Arg	Phe	Gly	Lys	Leu	Pro	Leu	Cys	Leu	Phe	Ile	Cys	Ile	Ile	Leu	
		35					40					45				

acg gcg gtg act gtg gta acc acg gcg cac cat acc cgt tta ctg acc 192
Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr
50 55 60

gct cag cgc gaa caa ctg gtg ctg gag cga gat gct tta gac att gaa 240

Ala	Gln	Arg	Glu	Gln	Leu	Val	Leu	Glu	Arg	Asp	Ala	Leu	Asp	Ile	Glu	
65					70					75					80	
tgg	cgc	aac	ctg	atc	ctt	gaa	gag	aat	gcg	ctc	ggc	gac	cat	agc	cgg	288
Trp	Arg	Asn	Leu	Ile	Leu	Glu	Glu	Asn	Ala	Leu	Gly	Asp	His	Ser	Arg	
			85						90					95		
gtg	gaa	agg	atc	gcc	acg	gaa	aag	ctg	caa	atg	cag	cat	gtt	gat	ccg	336
Val	Glu	Arg	Ile	Ala	Thr	Glu	Lys	Leu	Gln	Met	Gln	His	Val	Asp	Pro	
			100					105					110			
tca	caa	gaa	aat	atc	gta	gtg	caa	aaa	taa							366
Ser	Gln	Glu	Asn	Ile	Val	Val	Gln	Lys	*							
		115					120									

<210> 255
 <211> 1767
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1767)

<400> 255																
atg	aaa	gca	gcg	gcg	aaa	acg	cag	aaa	cca	aaa	cgt	cag	gaa	gaa	cat	48
Met	Lys	Ala	Ala	Ala	Lys	Thr	Gln	Lys	Pro	Lys	Arg	Gln	Glu	Glu	His	
1				5					10					15		
gcc	aac	ttt	atc	agt	tgg	cgt	ttt	gcg	ttg	tta	tgc	ggc	tgt	att	ctc	96
Ala	Asn	Phe	Ile	Ser	Trp	Arg	Phe	Ala	Leu	Leu	Cys	Gly	Cys	Ile	Leu	
			20					25					30			
ctg	gcg	ctg	gct	ttt	ctg	ctc	gga	cgc	gta	gcg	tgg	tta	caa	gtt	atc	144
Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gly	Arg	Val	Ala	Trp	Leu	Gln	Val	Ile	
		35					40					45				
tcc	ccg	gat	atg	ctg	gtg	aaa	gag	ggc	gac	atg	cgt	tct	ctt	cgc	gtt	192
Ser	Pro	Asp	Met	Leu	Val	Lys	Glu	Gly	Asp	Met	Arg	Ser	Leu	Arg	Val	
	50					55				60						
cag	caa	gtt	tcc	acc	tcc	cgc	ggc	atg	att	act	gac	cgt	tct	ggg	cgc	240
Gln	Gln	Val	Ser	Thr	Ser	Arg	Gly	Met	Ile	Thr	Asp	Arg	Ser	Gly	Arg	
65					70					75					80	
ccg	tta	gcg	gtg	agc	gtg	ccg	gta	aaa	gcg	att	tgg	gct	gac	ccg	aaa	288
Pro	Leu	Ala	Val	Ser	Val	Pro	Val	Lys	Ala	Ile	Trp	Ala	Asp	Pro	Lys	
			85						90					95		
gaa	gtg	cat	gac	gct	ggc	ggg	atc	agc	gtc	ggg	gac	cgc	tgg	aag	gcg	336
Glu	Val	His	Asp	Ala	Gly	Gly	Ile	Ser	Val	Gly	Asp	Arg	Trp	Lys	Ala	
			100				105						110			
ctg	gct	aac	gcg	ctc	aat	att	ccg	ctg	gat	cag	ctt	tca	gcc	cgc	att	384
Leu	Ala	Asn	Ala	Leu	Asn	Ile	Pro	Leu	Asp	Gln	Leu	Ser	Ala	Arg	Ile	
		115					120					125				

acc	ggg	gta	tta	cag	aag	tcg	agt	aac	gtc	ggg	ggt	tcc	aag	ctg	gcg	1104
Thr	Gly	Val	Leu	Gln	Lys	Ser	Ser	Asn	Val	Gly	Val	Ser	Lys	Leu	Ala	
		355					360					365				
tta	gcg	atg	ccg	tcc	tca	gcg	tta	gta	gat	act	tac	tca	cgt	ttt	gga	1152
Leu	Ala	Met	Pro	Ser	Ser	Ala	Leu	Val	Asp	Thr	Tyr	Ser	Arg	Phe	Gly	
		370					375					380				
ctg	gga	aaa	gcg	acc	aat	ttg	ggg	ttg	gtc	gga	gaa	cgc	agt	ggc	tta	1200
Leu	Gly	Lys	Ala	Thr	Asn	Leu	Gly	Leu	Val	Gly	Glu	Arg	Ser	Gly	Leu	
		385					390					395			400	
tat	cct	caa	aaa	caa	cgg	tgg	tct	gac	ata	gag	agg	gcc	acc	ttc	tct	1248
Tyr	Pro	Gln	Lys	Gln	Arg	Trp	Ser	Asp	Ile	Glu	Arg	Ala	Thr	Phe	Ser	
		405							410					415		
ttc	ggc	tac	ggg	cta	atg	gta	aca	cca	tta	cag	tta	gcg	cga	gtc	tac	1296
Phe	Gly	Tyr	Gly	Leu	Met	Val	Thr	Pro	Leu	Gln	Leu	Ala	Arg	Val	Tyr	
		420							425					430		
gca	act	atc	ggc	agc	tac	ggc	att	tat	cgc	cca	ctg	tcg	att	acc	aaa	1344
Ala	Thr	Ile	Gly	Ser	Tyr	Gly	Ile	Tyr	Arg	Pro	Leu	Ser	Ile	Thr	Lys	
		435							440					445		
gtt	gac	ccc	ccg	gtt	ccc	ggt	gaa	cgt	gtc	ttc	ccg	gaa	tcc	att	gtc	1392
Val	Asp	Pro	Pro	Val	Pro	Gly	Glu	Arg	Val	Phe	Pro	Glu	Ser	Ile	Val	
		450											460			
cgc	act	gtg	gtg	cat	atg	atg	gaa	agc	gtg	gcg	cta	cca	ggc	ggc	ggc	1440
Arg	Thr	Val	Val	His	Met	Met	Glu	Ser	Val	Ala	Leu	Pro	Gly	Gly	Gly	
		465											475			480
ggc	gtg	aag	gcg	gcg	att	aaa	ggc	tat	cgt	atc	gcc	att	aaa	acc	ggt	1488
Gly	Val	Lys	Ala	Ala	Ile	Lys	Gly	Tyr	Arg	Ile	Ala	Ile	Lys	Thr	Gly	
		485											490			495
acc	gcg	aaa	aag	gtc	ggg	ccg	gac	ggt	cgc	tac	atc	aat	aaa	tat	att	1536
Thr	Ala	Lys	Lys	Val	Gly	Pro	Asp	Gly	Arg	Tyr	Ile	Asn	Lys	Tyr	Ile	
		500											510			
gct	tat	acc	gca	ggc	gtt	gcg	cct	gcg	agt	cag	ccg	cgc	ttc	gcg	ctg	1584
Ala	Tyr	Thr	Ala	Gly	Val	Ala	Pro	Ala	Ser	Gln	Pro	Arg	Phe	Ala	Leu	
		515											525			
gtt	gtt	gtt	atc	aac	gat	ccg	cag	gcg	ggt	aaa	tac	tac	ggc	ggc	gcc	1632
Val	Val	Val	Ile	Asn	Asp	Pro	Gln	Ala	Gly	Lys	Tyr	Tyr	Gly	Gly	Ala	
		530											540			
gtt	tcc	gcg	ccg	gtc	ttt	ggt	gcc	atc	atg	ggc	ggc	gta	ttg	cgt	acc	1680
Val	Ser	Ala	Pro	Val	Phe	Gly	Ala	Ile	Met	Gly	Gly	Val	Leu	Arg	Thr	
		545											555			560
atg	aac	atc	gag	ccg	gat	gcg	ctg	aca	acg	ggc	gat	aaa	aat	gaa	ttt	1728
Met	Asn	Ile	Glu	Pro	Asp	Ala	Leu	Thr	Thr	Gly						

Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser *
 580 585

<210> 256
 <211> 1488
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1488)

<400> 256
 gtg gca gat cgt aat ttg cgc gac ctt ctt gct ccg tgg gtg cca gac 48
 Met Ala Asp Arg Asn Leu Arg Asp Leu Leu Ala Pro Trp Val Pro Asp
 1 5 10 15
 gca cct tcg cga gca ctg cga gag atg aca ctc gac agc cgt gtg gct 96
 Ala Pro Ser Arg Ala Leu Arg Glu Met Thr Leu Asp Ser Arg Val Ala
 20 25 30
 gcg gcg ggc gat ctc ttt gta gct gta gta ggt cat cag gcg gac ggg 144
 Ala Ala Gly Asp Leu Phe Val Ala Val Val Gly His Gln Ala Asp Gly
 35 40 45
 cgt cga tat atc ccg cag gcg ata gcg caa ggt gtg gct gcc att att 192
 Arg Arg Tyr Ile Pro Gln Ala Ile Ala Gln Gly Val Ala Ala Ile Ile
 50 55 60
 gca gag gcg aaa gat gag gcg acc gat ggt gaa atc cgt gaa atg cac 240
 Ala Glu Ala Lys Asp Glu Ala Thr Asp Gly Glu Ile Arg Glu Met His
 65 70 75 80
 ggc gta ccg gtc atc tat ctc agc cag ctc aac gag cgt tta tct gca 288
 Gly Val Pro Val Ile Tyr Leu Ser Gln Leu Asn Glu Arg Leu Ser Ala
 85 90 95
 ctg gcg ggc cgc ttt tac cat gaa ccc tct gac aat tta cgt ctc gtg 336
 Leu Ala Gly Arg Phe Tyr His Glu Pro Ser Asp Asn Leu Arg Leu Val
 100 105 110
 ggc gta acg ggc acc aac ggc aaa acc acg act acc cag ctg ttg gcg 384
 Gly Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr Gln Leu Leu Ala
 115 120 125
 cag tgg agc caa ctg ctt ggc gaa atc agc gcg gta atg ggc acc gtt 432
 Gln Trp Ser Gln Leu Leu Gly Glu Ile Ser Ala Val Met Gly Thr Val
 130 135 140
 ggt aac ggc ctg ctg ggg aaa gtg atc ccg aca gaa aat aca acc ggt 480
 Gly Asn Gly Leu Leu Gly Lys Val Ile Pro Thr Glu Asn Thr Thr Gly
 145 150 155 160
 tcg gca gtc gat gtt cag cat gag ctg gcg ggg ctg gtg gat cag ggc 528
 Ser Ala Val Asp Val Gln His Glu Leu Ala Gly Leu Val Asp Gln Gly
 165 170 175

305	310	315	320	
caa ctg gca gaa aac cag ttg ctg ctc gac gac tcc tac aac gcc aat				1008
Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn				
	325	330	335	
gtc ggt tca atg act gca gca gtc cag gta ctg gct gaa atg ccg ggc				1056
Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly				
	340	345	350	
tac cgc gtg ctg gtg gtg ggc gat atg gcg gaa ctg ggc gct gaa agc				1104
Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser				
	355	360	365	
gaa gcc tgc cat gta cag gtg ggc gag gcg gca aaa gct gct ggt att				1152
Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile				
	370	375	380	
gac cgc gtg tta agc gtg ggt aaa caa agc cat gct atc agc acc gcc				1200
Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala				
	385	390	395	400
agc ggc gtt ggc gaa cat ttt gct gat aaa act gcg tta att acg cgt				1248
Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg				
	405	410	415	
ctt aaa tta ctg att gct gag caa cag gta att acg att tta gtt aag				1296
Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys				
	420	425	430	
ggc tca cgt agt gcc gcc atg gaa gag gta gta cgc gct tta cag gag				1344
Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu				
	435	440	445	
aat ggg aca tgt tag				1359
Asn Gly Thr Cys *				
	450			

<210> 258
 <211> 1083
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(1083)

<400> 258	
atg tta gtt tgg ctg gcc gaa cat ttg gtc aaa tat tat tcc ggc ttt	48
Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe	
1 5 10 15	
aac gtc ttt tcc tat ctg acg ttt cgc gcc atc gtc agc ctg ctg acc	96
Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr	
20 25 30	

gcg Ala	ctg Leu	ttc Phe 35	atc Ile	tca Ser	ttg Leu	tgg Trp	atg Met 40	ggc Gly	ccg Pro	cgt Arg	atg Met	att Ile 45	gct Ala	cat His	ttg Leu	144
caa Gln	aaa Lys 50	ctt Leu	tcc Ser	ttt Phe	ggg Gly 55	cag Gln	gtg Val	gtg Val	cgt Arg	aac Asn	gac Asp 60	ggg Gly	cct Pro	gaa Glu	tca Ser	192
cac His 65	ttc Phe	agc Ser	aag Lys	cgc Arg	ggg Gly 70	acg Thr	ccg Pro	acc Thr	atg Met	ggc Gly 75	ggg Gly	att Ile	atg Met	atc Ile	ctg Leu 80	240
acg Thr	gcg Ala	att Ile	gtg Val	atc Ile 85	tcc Ser	gta Val	ctg Leu	ctg Leu	tgg Trp 90	gct Ala	tac Tyr	ccg Pro	tcc Ser	aat Asn 95	ccg Pro	288
tac Tyr	gtc Val	tgg Trp 100	tgc Cys	gtg Val	ttg Leu	gtg Val	gtg Val	ctg Leu 105	gta Val	ggg Gly	tac Tyr	ggg Gly 110	gtt Val	att Ile	ggc Gly	336
ttt Phe	gtt Val 115	gat Asp	gat Asp	tat Tyr	cgc Arg	aaa Lys 120	gtg Val	gtg Val	cgt Arg	aaa Lys	gac Asp 125	acc Thr	aaa Lys	ggg Gly	ttg Leu	384
atc Ile 130	gct Ala	cgt Arg	tgg Trp	aag Lys	tat Tyr	ttc Phe 135	tgg Trp	atg Met	tcg Ser	gtc Val	att Ile 140	gcg Ala	ctg Leu	ggg Gly	gtc Val	432
gcc Ala 145	ttc Phe	gcc Ala	ctg Leu	tac Tyr	ctt Leu 150	gcc Ala	ggc Gly	aaa Lys	gac Asp 155	acg Thr	ccc Pro	gca Ala	acg Thr	cag Gln	ctg Leu 160	480
gtg Val	gtc Val	cca Pro	ttc Phe 165	ttt Phe	aaa Lys	gat Asp	gtg Val	atg Met	ccg Pro 170	cag Gln	ctg Leu	ggg Gly	ctg Leu	ttc Phe 175	tac Tyr	528
att Ile	ctg Leu	ctg Leu	gct Ala 180	tac Tyr	ttc Phe	gtc Val	att Ile	gtg Val 185	ggg Gly	act Thr	ggc Gly	aac Asn 190	gcg Ala	gta Val	aac Asn	576
ctg Leu	acc Thr 195	gat Asp	ggg Gly	ctc Leu	gac Asp	ggc Gly 200	ctg Leu	gca Ala	att Ile	atg Met	ccg Pro 205	acc Thr	gta Val	ttt Phe	gtc Val	624
gcc Ala 210	ggg Gly	ggg Gly	ttt Phe	gcg Ala	ctg Leu 215	gtg Val	gcg Ala	tgg Trp	gcg Ala	acc Thr	ggc Gly 220	aac Asn	atg Met	aac Asn	ttt Phe	672
gcc Ala 225	agc Ser	tac Tyr	ttg Leu	cat His 230	ata Ile	ccg Pro	tat Tyr	ctg Leu	cga Arg	cac His 235	gcc Ala	ggg Gly	gaa Glu	ctg Leu	gtt Val 240	720
att Ile	gtc Val	tgt Cys	acc Thr 245	gcg Ala	ata Ile	gtc Val	ggg Gly	gca Ala	gga Gly 250	ctg Leu	ggc Gly	ttc Phe	ctg Leu	tgg Trp 255	ttt Phe	768
aac	acc	tat	ccg	gcg	cag	gtc	ttt	atg	ggc	gat	gta	ggg	tcg	ctg	gcg	816

Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
260 265 270

tta	ggt	ggt	gcg	tta	ggc	att	atc	gcc	gta	ctg	cta	cgt	cag	gaa	ttc	864
Leu	Gly	Gly	Ala	Leu	Gly	Ile	Ile	Ala	Val	Leu	Leu	Arg	Gln	Glu	Phe	
		275					280					285				

ctg	ctg	gtg	att	atg	ggg	ggc	gtg	ttc	gtg	gta	gaa	acg	ctt	tct	gtc	912
Leu	Leu	Val	Ile	Met	Gly	Gly	Val	Phe	Val	Val	Glu	Thr	Leu	Ser	Val	
	290					295					300					

atc	ctg	cag	gtc	ggc	tcc	ttt	aaa	ctg	cgc	gga	caa	cgt	att	ttc	cgc	960
Ile	Leu	Gln	Val	Gly	Ser	Phe	Lys	Leu	Arg	Gly	Gln	Arg	Ile	Phe	Arg	
305					310					315					320	

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atg gca ccg att cat cac cac tat gaa ctg aaa ggc tgg ccg gaa ccg    1008
Met Ala Pro Ile His His His Tyr Glu Leu Lys Gly Trp Pro Glu Pro
          325                      330                      335

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cgc gtc att gtg cgt ttc tgg att att tcg ctg atg ctg gtt ctg att 1056
Arg Val Ile Val Arg Phe Trp Ile Ile Ser Leu Met Leu Val Leu Ile
340 345 350

ggt ctg gca acg ctg aag gta cgt taa 1083
Gly Leu Ala Thr Leu Lys Val Arg *
355 360

<210> 259

<211> 1317

<212> DNA

<213> Escherichia coli

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1317)$

<400> 259

atg gct gat tat cag ggt aaa aat gtc gtc att atc ggc ctg ggc ctc 48
Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu
1 5 10 15

acc ggg ctt tcc tgc gtg gac ttt ttc ctc gct cgc ggt gtg acg ccg 96
Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro
20 25 30

cgc gtt atg gat acg cgt atg aca ccg cct ggc ctg gat aaa tta ccc 144
 Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
 35 40 45

gaa gcc gta gaa cgc cac acg ggc agt ctg aat gat gaa tgg ctg atg 192
Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
50 55 60

gcg gca gat ctg att gtc gcc agt ccc ggt att gca ctg gcg cat cca 240
Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
65 70 75 80

tcc tta agc gct gcc gct gat gcc gga atc gaa atc gtt ggc gat atc	288
Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile	
85 90 95	
gag ctg ttc tgt cgc gaa gca caa gca ccg att gtg gcg att acc ggt	336
Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly	
100 105 110	
tct aac ggc aaa agc acg gtc acc acg cta gtg ggt gaa atg gcg aaa	384
Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys	
115 120 125	
gcg gcg ggg gtt aac gtt ggt gtg ggt ggc aat att ggc ctg cct gcg	432
Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala	
130 135 140	
ttg atg cta ctg gat gat gag tgt gaa ctg tac gtg ctg gaa ctg tcg	480
Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser	
145 150 155 160	
agc ttc cag ctg gaa acc acc tcc agc tta cag gcg gta gca gcg acc	528
Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr	
165 170 175	
att ctg aac gtg act gaa gat cat atg gat cgc tat ccg ttt ggt tta	576
Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu	
180 185 190	
caa cag tat cgt gca gca aaa ctg cgc att tac gaa aac gcg aaa gtt	624
Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val	
195 200 205	
tgc gtg gtt aat gct gat gat gcc tta aca atg ccg att cgc ggt gcg	672
Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala	
210 215 220	
gat gaa cgc tgc gtc agc ttt ggc gtc aac atg ggt gac tat cac ctg	720
Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu	
225 230 235 240	
aat cat cag cag ggc gaa acc tgg ctg cgg gtt aaa ggc gag aaa gtg	768
Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val	
245 250 255	
ctg aat gtg aaa gag atg aaa ctt tcc ggg cag cat aac tac acc aat	816
Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn	
260 265 270	
gcg ctg gcg gcg ctg gcg ctg gca gat gct gca ggg tta ccg cgt gcc	864
Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala	
275 280 285	
agc agc ctg aaa gcg tta acc aca ttc act ggt ctg ccg cat cgc ttt	912
Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe	
290 295 300	

gaa gtt gtg ctg gag cat aac ggc gta cgt tgg att aac gat tcg aaa	960
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys	
305 310 315 320	
gcg acc aac gtc ggc agt acg gaa gcg gcg ctg aat ggc ctg cac gta	1008
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val	
325 330 335	
gac ggc aca ctg cat ttg ttg ctg ggt ggc gat ggt aaa tcg gcg gac	1056
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp	
340 345 350	
ttt agc cca ctg gcg cgt tac ctg aat ggc gat aac gta cgt ctg tat	1104
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr	
355 360 365	
tgt ttc ggt cgt gac ggc gcg cag ctg gcg gcg cta cgc ccg gaa gtg	1152
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val	
370 375 380	
gca gaa caa acc gaa act atg gaa cag gcg atg cgc ttg ctg gct ccg	1200
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro	
385 390 395 400	
cgt gtt cag ccg ggc gat atg gtt ctg ctc tcc cca gcc tgt gcc agc	1248
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser	
405 410 415	
ctt gat cag ttc aag aac ttt gaa caa cga ggc aat gag ttt gcc cgt	1296
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg	
420 425 430	
ctg gcg aag gag tta ggt tga	1317
Leu Ala Lys Glu Leu Gly *	
435	

<210> 260

<211> 1245

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1245)

<400> 260

atg cgt tta tct ctc cct cgc ctg aaa atg ccg cgc ctg cca gga ttc	48
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe	
1 5 10 15	

agt atc ctg gtc tgg atc tcc acg gcg cta aag ggc tgg gtg atg ggc	96
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly	
20 25 30	

tcg cgg gaa aaa gat acc gac agc ctg atc atg tac gat cgc acc tta	144
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu	

45

ccc ttt ggc agc ggc tat cag tta acg caa tgc ctg atg gcg ttt ggt 816
Pro Phe Gly Ser Gly Tyr Gln Leu Thr Gln Ser Leu Met Ala Phe Gly
260 265 270

Val	Val	Cys	Arg	Ser	Gly	Ala	Leu	Thr	Val	Ser	Glu	Ile	Ala	Ala	Ala		
			260					265					270				
gga	cta	ccg	gcg	ttg	ttt	gtg	ccg	ttt	caa	cat	aaa	gac	cgc	cag	caa	864	
Gly	Leu	Pro	Ala	Leu	Phe	Val	Pro	Phe	Gln	His	Lys	Asp	Arg	Gln	Gln		
		275					280					285					
tac	tgg	aat	gcg	cta	ccg	ctg	gaa	aaa	gcg	ggc	gca	gcc	aaa	att	atc	912	
Tyr	Trp	Asn	Ala	Leu	Pro	Leu	Glu	Lys	Ala	Gly	Ala	Ala	Lys	Ile	Ile		
	290					295					300						
gag	cag	cca	cag	ctt	agc	gtg	gat	gct	gtc	gcc	aac	acc	ctg	gcc	ggg	960	
Glu	Gln	Pro	Gln	Leu	Ser	Val	Asp	Ala	Val	Ala	Asn	Thr	Leu	Ala	Gly		
305					310					315					320		
tgg	tcg	cga	gaa	acc	tta	tta	acc	atg	gca	gaa	cgc	gcc	cgc	gct	gca	1008	
Trp	Ser	Arg	Glu	Thr	Leu	Leu	Thr	Met	Ala	Glu	Arg	Ala	Arg	Ala	Ala		
			325						330					335			
tcc	att	ccg	gat	gcc	acc	gag	cga	gtg	gca	aat	gaa	gtg	agc	cgg	gtt	1056	
Ser	Ile	Pro	Asp	Ala	Thr	Glu	Arg	Val	Ala	Asn	Glu	Val	Ser	Arg	Val		
			340					345					350				
gcc	cgg	gcg	taa													1068	
Ala	Arg	Ala	*														
		355															
<210>	262																
<211>	1476																
<212>	DNA																
<213>	Escherichia coli																
<220>																	
<221>	CDS																
<222>	(1)...(1476)																
<400>	262																
atg	aat	aca	caa	caa	ttg	gca	aaa	ctg	cgt	tcc	atc	gtg	ccc	gaa	atg	48	
Met	Asn	Thr	Gln	Gln	Leu	Ala	Lys	Leu	Arg	Ser	Ile	Val	Pro	Glu	Met		
1				5				10					15				
cgt	cgc	gtt	cgg	cac	ata	cat	ttt	gtc	ggc	att	ggg	ggg	gcc	ggg	atg	96	
Arg	Arg	Val	Arg	His	Ile	His	Phe	Val	Gly	Ile	Gly	Gly	Ala	Gly	Met		
			20					25					30				
ggc	ggg	att	gcc	gaa	gtt	ctg	gcc	aat	gaa	ggg	tat	cag	atc	agt	ggg	144	
Gly	Gly	Ile	Ala	Glu	Val	Leu	Ala	Asn	Glu	Gly	Tyr	Gln	Ile	Ser	Gly		
		35				40						45					
tcc	gat	tta	gcg	cca	aat	ccg	gtc	acg	cag	cag	tta	atg	aat	ctg	ggg	192	
Ser	Asp	Leu	Ala	Pro	Asn	Pro	Val	Thr	Gln	Gln	Leu	Met	Asn	Leu	Gly		
	50					55					60						
gcg	acg	att	tat	ttc	aac	cat	cgc	ccg	gaa	aac	gta	cgt	gat	gcc	agc	240	
Ala	Thr	Ile	Tyr	Phe	Asn	His	Arg	Pro	Glu	Asn	Val	Arg	Asp	Ala	Ser		
65				70				75							80		

acg gaa gag ggc att gac gac gag gct att ttg cgg gcg ctt gaa agc	960
Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser	
305 310 315 320	
ttc cag ggg act ggt cgc cgt ttt gat ttc ctc ggt gaa ttc ccg ctg	1008
Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu	
325 330 335	
gag cca gtg aat ggt aaa agc ggt acg gca atg ctg gtc gat gac tac	1056
Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr	
340 345 350	
ggc cac cac ccg acg gaa gtg gac gcc acc att aaa gcg gcg cgc gca	1104
Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala	
355 360 365	
ggc tgg ccg gat aaa aac ctg gta atg ctg ttt cag ccg cac cgt ttt	1152
Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe	
370 375 380	
acc cgt acg cgc gac ctg tat gat gat ttc gcc aat gtg ctg acg cag	1200
Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln	
385 390 395 400	
gtt gat acc ctg ttg atg ctg gaa gtg tat ccg gct ggc gaa gcg cca	1248
Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro	
405 410 415	
att ccg gga gcg gac agc cgt tgc ctg tgt cgc aca att cgt gga cgt	1296
Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg	
420 425 430	
ggg aaa att gat ccc att ctg gtg ccg gat ccg gcg cgg gta gcc gag	1344
Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu	
435 440 445	
atg ctg gca ccg gta tta acc ggt aac gac ctg att ctc gtt cag ggg	1392
Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly	
450 455 460	
gct ggt aat att gga aaa att gcc cgt tct tta gct gaa atc aaa ctg	1440
Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu	
465 470 475 480	
aag ccg caa act ccg gag gaa gaa caa cat gac tga	1476
Lys Pro Gln Thr Pro Glu Glu Glu Gln His Asp *	
485 490	

<210> 263
 <211> 921
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(921)

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290295300																
gga Gly	gaa Glu	gcg Ala	atc Ile	acc Thr	ctg Leu	gtg Val	ctg Leu	acg Thr	gat Asp	gag Glu	atc Ile	gac Asp	atc Ile	agc Ser	cgt Arg	960
305310315320																
ggc Gly	gat Asp	ctg Leu	ctg Leu	ctg Leu	gcg Ala	gca Ala	gac Asp	gaa Glu	gcg Ala	tta Leu	ccg Pro	gcg Ala	gtg Val	cag Gln	agc Ser	1008
325330335																
gcg Ala	tcg Ser	gtg Val	gat Asp	gtg Val	gta Val	tgg Trp	atg Met	gcg Ala	gaa Glu	cag Gln	ccg Pro	ctt Leu	tct Ser	cca Pro	ggg Gly	1056
340345350																
cag Gln	agt Ser	tac Tyr	gac Asp	atc Ile	aaa Lys	att Ile	gcc Ala	ggt Gly	aag Lys	aag Lys	acg Thr	cgc Arg	gcg Ala	cgt Arg	gtt Val	1104
355360365																
gat Asp	ggc Gly	att Ile	cgc Arg	tat Tyr	cag Gln	gtt Val	gat Asp	att Ile	aat Asn	aac Asn	ctt Leu	acc Thr	cag Gln	cgt Arg	gaa Glu	1152
370375380																
gtt Val	gaa Glu	aac Asn	ctg Leu	cca Pro	ctg Leu	aat Asn	ggg Gly	atc Ile	ggc Gly	ctc Leu	gtg Val	gat Asp	ctc Leu	act Thr	ttt Phe	1200
385390395400																
gac Asp	gag Glu	ccg Pro	ctg Leu	gtg Val	tta Leu	gat Asp	cgt Arg	tat Tyr	caa Gln	caa Gln	aat Asn	ccg Pro	gtg Val	acg Thr	ggt Gly	1248
405410415																
ggg Gly	ctg Leu	att Ile	ttt Phe	atc Ile	gat Asp	cgc Arg	ctg Leu	agc Ser	aat Asn	gtg Val	acc Thr	gtg Val	ggt Gly	gcc Ala	ggt Gly	1296
420425430																
atg Met	gtg Val	cac His	gag Glu	cca Pro	gtt Val	agc Ser	cag Gln	gca Ala	act Thr	gct Ala	gcg Ala	cca Pro	tct Ser	gaa Glu	ttc Phe	1344
435440445																
agt Ser	gca Ala	ttc Phe	gaa Glu	ctg Leu	gaa Glu	ttg Leu	aat Asn	gct Ala	ctg Leu	gtt Val	cgt Arg	cgc Arg	cac His	ttt Phe	ccg Pro	1392
450455460																
cac His	tgg Trp	ggc Gly	gcg Ala	cgc Arg	gat Asp	ttg Leu	ctg Leu	ggg Gly	gat Asp	aaa Lys	taa *					1428
465470475																

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<210> 266
<211> 384
<212> DNA
<213> Escherichia coli
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<400> 266

atg	cgc	cat	cgt	aag	agt	ggt	cgt	caa	ctg	aac	cgc	aac	agc	agc	cat	48
Met	Arg	His	Arg	Lys	Ser	Gly	Arg	Gln	Leu	Asn	Arg	Asn	Ser	Ser	His	
1				5					10					15		

cgc	cag	gct	atg	ttc	cgc	aat	atg	gca	ggt	tca	ctg	ggt	cgt	cat	gaa	96
Arg	Gln	Ala	Met	Phe	Arg	Asn	Met	Ala	Gly	Ser	Leu	Val	Arg	His	Glu	
			20					25					30			

atc	atc	aag	acg	act	ctg	cct	aaa	gcg	aaa	gag	ctg	cgc	cgc	gta	gtt	144
Ile	Ile	Lys	Thr	Thr	Leu	Pro	Lys	Ala	Lys	Glu	Leu	Arg	Arg	Val	Val	
		35					40					45				

gag	ccg	ctg	att	act	ctt	gcc	aag	act	gat	agc	ggt	gct	aat	cgt	cgt	192
Glu	Pro	Leu	Ile	Thr	Leu	Ala	Lys	Thr	Asp	Ser	Val	Ala	Asn	Arg	Arg	
	50					55					60					

ctg	gca	ttc	gcc	cgt	act	cgt	gat	aac	gag	atc	gtg	gca	aaa	ctg	ttt	240
Leu	Ala	Phe	Ala	Arg	Thr	Arg	Asp	Asn	Glu	Ile	Val	Ala	Lys	Leu	Phe	
65					70					75				80		

aac	gaa	ctg	ggc	ccg	cgt	ttc	gcg	agc	cgt	gcc	ggt	ggt	tac	act	cgt	288
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Ala	Ser	Arg	Ala	Gly	Gly	Tyr	Thr	Arg	
				85					90					95		

att	ctg	aag	tgt	ggc	ttc	cgt	gca	ggc	gac	aac	gcg	ccg	atg	gct	tac	336
Ile	Leu	Lys	Cys	Gly	Phe	Arg	Ala	Gly	Asp	Asn	Ala	Pro	Met	Ala	Tyr	
		100						105					110			

atc	gag	ctg	ggt	gat	cgt	tca	gag	aaa	gca	gaa	gct	gct	gca	gag	taa	384
Ile	Glu	Leu	Val	Asp	Arg	Ser	Glu	Lys	Ala	Glu	Ala	Ala	Ala	Glu	*	
		115					120					125				

<210> 267

<211> 990

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(990)

<400> 267

atg	cag	ggt	tct	gtg	aca	gag	ttt	cta	aaa	ccg	cgc	ctg	ggt	gat	atc	48
Met	Gln	Gly	Ser	Val	Thr	Glu	Phe	Leu	Lys	Pro	Arg	Leu	Val	Asp	Ile	
1				5					10					15		

gag	caa	gtg	agt	tcg	acg	cac	gcc	aag	gtg	acc	ctt	gag	cct	tta	gag	96
Glu	Gln	Val	Ser	Ser	Thr	His	Ala	Lys	Val	Thr	Leu	Glu	Pro	Leu	Glu	
			20					25					30			

cgt	ggc	ttt	ggc	cat	act	ctg	ggt	aac	gca	ctg	cgc	cgt	att	ctg	ctc	144
Arg	Gly	Phe	Gly	His	Thr	Leu	Gly	Asn	Ala	Leu	Arg	Arg	Ile	Leu	Leu	
		35					40					45				

tca tgc atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta	192
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val	
50 55 60	
cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa	240
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu	
65 70 75 80	
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat	288
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp	
85 90 95	
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca	336
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala	
100 105 110	
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac	384
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His	
115 120 125	
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc	432
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile	
130 135 140	
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat	480
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His	
145 150 155 160	
tgc gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc	528
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys	
165 170 175	
tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta	576
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val	
180 185 190	
gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac	624
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn	
195 200 205	
ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg	672
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu	
210 215 220	
gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct	720
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro	
225 230 235 240	
gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct	768
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro	
245 250 255	
gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca	816
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala	
260 265 270	

gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag	864
Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu	
275 280 285	

ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa	912
Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys	
290 295 300	

gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac	960
Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn	
305 310 315 320	

tgg cca ccg gca agc atc gct gac gag taa	990
Trp Pro Pro Ala Ser Ile Ala Asp Glu *	
325	

<210> 268
 <211> 621
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(621)

<400> 268	
atg gca aga tat ttg ggt cct aag ctg aag ctg agc cgt cgt gag ggc	48
Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly	
1 5 10 15	

acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt	96
Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys	
20 25 30	

aaa att gaa caa gct cct ggc cag cac ggt gcg cgt aaa ccg cgt ctg	144
Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu	
35 40 45	

tct gac tat ggt gtg cag ttg cgt gaa aag caa aaa gtt cgc cgt atc	192
Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile	
50 55 60	

tat ggt gtg ctg gag cgt cag ttc cgt aac tac tac aaa gaa gca gca	240
Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala	
65 70 75 80	

cgt ctg aaa ggc aac acc ggt gaa aac ctg ttg gct ctg ctg gaa ggt	288
Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly	
85 90 95	

cgt ctg gac aac gtt gta tac cgt atg ggc ttc ggt gcc act cgt gca	336
Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala	
100 105 110	

gaa gca cgt cag ctg gtt agc cat aaa gca att atg gta aac ggt cgt	384
Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg	

115	120	125	
ggt ggt aac atc gct tct tat cag gtt agt ccg aat gac gtt gta agc			432
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser			
130	135	140	
att cgt gag aaa gcg aag aag cag tct cgc gtg aaa gcc gct ctg gag			480
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu			
145	150	155	160
ctg gct gag cag cgt gaa aag cca acc tgg ctg gaa gtt gat gct ggc			528
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly			
165	170	175	
aag atg gaa ggt acg ttt aag cgt aag ccg gag cgt tct gat ctg tct			576
Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser			
180	185	190	
gcg gac att aac gaa cac ctg atc gtc gag ctt tac tcc aag taa			621
Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys *			
195	200	205	

<210> 269
 <211> 390
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(390)

<400> 269	
atg gca aag gca cca att cgt gca cgt aaa cgt gta aga aaa caa gtc	48
Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val	
1 5 10 15	
tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg	96
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val	
20 25 30	
act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt	144
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly	
35 40 45	
ggt tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag	192
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln	
50 55 60	
ggt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag	240
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys	
65 70 75 80	
aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act	288
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr	
85 90 95	

att cgt gct ctg aac gcc gca ggt ttc cgc atc act aac att act gat	336
Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp	
100 105 110	
gtg act ccg atc cct cat aac ggt tgt cgt ccg ccg aaa aaa cgt cgc	384
Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg	
115 120 125	
gta taa	390
Val *	

<210> 270
 <211> 357
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(357)

<400> 270	
gtg gcc cgt ata gca ggc att aac att cct gat cat aag cat gcc gta	48
Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val	
1 5 10 15	
atc gca tta act tcg att tat ggc gtc ggc aag acc cgt tct aaa gcc	96
Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala	
20 25 30	
atc ctg gct gca gcg ggt atc gct gaa gat gtt aag atc agt gag ctg	144
Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu	
35 40 45	
tct gaa gga caa atc gac acg ctg cgt gac gaa gtt gcc aaa ttt gtc	192
Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val	
50 55 60	
gtt gaa ggt gat ctg cgc cgt gaa atc agc atg agc atc aag cgc ctg	240
Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu	
65 70 75 80	
atg gat ctt ggt tgc tat cgc ggt ttg cgt cat cgt cgt ggt ctc ccg	288
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro	
85 90 95	
gtt cgc ggt cag cgt acc aag acc aac gca cgt acc cgt aag ggt ccg	336
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro	
100 105 110	
cgc aaa ccg atc aag aaa taa	357
Arg Lys Pro Ile Lys Lys *	
115	

<210> 271
 <211> 1383
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1383)

<400> 271

atg acg caa tta acc atg aaa gac aaa att ggc tac ggg ctg gga gac	48
Met Thr Gln Leu Thr Met Lys Asp Lys Ile Gly Tyr Gly Leu Gly Asp	
1 5 10 15	
acc gcc tgc ggc ttc gtc tgg cag gcc acg atg ttc ctg ctg gcc tat	96
Thr Ala Cys Gly Phe Val Trp Gln Ala Thr Met Phe Leu Leu Ala Tyr	
20 25 30	
ttc tac acc gac gtc ttc ggc ctg tcg gcg ggg att atg ggc acg ctg	144
Phe Tyr Thr Asp Val Phe Gly Leu Ser Ala Gly Ile Met Gly Thr Leu	
35 40 45	
ttt ttg gtc tcc cgc gtg ctc gac gcc gtc acc gac ccg ctg atg ggg	192
Phe Leu Val Ser Arg Val Leu Asp Ala Val Thr Asp Pro Leu Met Gly	
50 55 60	
ctg ctg gta gac cgc acc cgc acg ccg cac ggc cag ttc cgc ccg ttc	240
Leu Leu Val Asp Arg Thr Arg Thr Arg His Gly Gln Phe Arg Pro Phe	
65 70 75 80	
ctg ctg tgg ggg gcc atc ccg ttc ggc atc gtc tgc gtg ctg acc ttc	288
Leu Leu Trp Gly Ala Ile Pro Phe Gly Ile Val Cys Val Leu Thr Phe	
85 90 95	
tac acg ccg gac ttc tcc gca cag ggc aag atc atc tac gcc tgc gtg	336
Tyr Thr Pro Asp Phe Ser Ala Gln Gly Lys Ile Ile Tyr Ala Cys Val	
100 105 110	
acc tac att ctc ctg acc ctg gtc tac acc ttc gtt aac gtg ccg tac	384
Thr Tyr Ile Leu Leu Thr Leu Val Tyr Thr Phe Val Asn Val Pro Tyr	
115 120 125	
tgc gcc atg ccg ggc gtc atc acc gcc gac ccg aaa gag cgt cac gcc	432
Cys Ala Met Pro Gly Val Ile Thr Ala Asp Pro Lys Glu Arg His Ala	
130 135 140	
ctg cag tcc tgg cgc ttc ttc ctg gcg gcg gcg ggc tcg ctc gct atc	480
Leu Gln Ser Trp Arg Phe Phe Leu Ala Ala Ala Gly Ser Leu Ala Ile	
145 150 155 160	
agc ggc atc gcg ctg ccg ctg gtg agc atc atc ggc aaa ggg gac gag	528
Ser Gly Ile Ala Leu Pro Leu Val Ser Ile Ile Gly Lys Gly Asp Glu	
165 170 175	
cag gtg ggc tac ttc ggc gcc atg tgc gtg ctg ggg ctg agc ggc gtg	576
Gln Val Gly Tyr Phe Gly Ala Met Cys Val Leu Gly Leu Ser Gly Val	
180 185 190	

gcg ggc atg ttc atc atg ctg tcg ctc tac aag ctc acc gat gcc cgc	1296
Ala Gly Met Phe Ile Met Leu Ser Leu Tyr Lys Leu Thr Asp Ala Arg	
420 425 430	
gtg gag gcc atc agc cgg cag ctg att aag cac cgc gcg gcg cag ggc	1344
Val Glu Ala Ile Ser Arg Gln Leu Ile Lys His Arg Ala Ala Gln Gly	
435 440 445	
gag gcc gtt ccc gac gcc gcg aca gcc gca tcc cat taa	1383
Glu Ala Val Pro Asp Ala Ala Thr Ala Ala Ser His *	
450 455 460	

<210> 272
 <211> 1611
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1611)

<400> 272	
atg gaa atc act aac ccg ata ctc acc ggc ttc aac ccg gac ccg tcc	48
Met Glu Ile Thr Asn Pro Ile Leu Thr Gly Phe Asn Pro Asp Pro Ser	
1 5 10 15	
ctg tgc cgc cag ggc gag gac tac tac atc gcc acc tcg acc ttc gag	96
Leu Cys Arg Gln Gly Glu Asp Tyr Tyr Ile Ala Thr Ser Thr Phe Glu	
20 25 30	
tgg ttc ccg ggc gtg cgc atc tac cac tcc cgt gac ctg aaa aac tgg	144
Trp Phe Pro Gly Val Arg Ile Tyr His Ser Arg Asp Leu Lys Asn Trp	
35 40 45	
tcg ctg gtc agc acc ccg ttg gac cgc gtg tcg atg ctg gac atg aag	192
Ser Leu Val Ser Thr Pro Leu Asp Arg Val Ser Met Leu Asp Met Lys	
50 55 60	
ggc aac ccg gac tcc ggc ggc atc tgg gcg ccg tgc ctg agc tac gcc	240
Gly Asn Pro Asp Ser Gly Gly Ile Trp Ala Pro Cys Leu Ser Tyr Ala	
65 70 75 80	
gac ggt aaa ttc tgg ctg ctc tac acc gac gtg aag att gtc gac tcg	288
Asp Gly Lys Phe Trp Leu Leu Tyr Thr Asp Val Lys Ile Val Asp Ser	
85 90 95	
ccg tgg aaa aac ggc cgc aac ttc ctc gtc acc gcg ccc tcc atc gag	336
Pro Trp Lys Asn Gly Arg Asn Phe Leu Val Thr Ala Pro Ser Ile Glu	
100 105 110	
ggg cca tgg agc gag cca atc ccg atg ggc aac ggc ggg ttt gac ccg	384
Gly Pro Trp Ser Glu Pro Ile Pro Met Gly Asn Gly Gly Phe Asp Pro	
115 120 125	
tcc ctg ttc cac gac gac gat ggc cgc aaa tac tat atc tac cgc ccg	432
Ser Leu Phe His Asp Asp Asp Gly Arg Lys Tyr Tyr Ile Tyr Arg Pro	

ggc Gly	aac Asn 370	gac Asp	tcg Ser	ctc Leu	aat Asn 375	tcg Ser	acc Thr	ttc Phe	acc Thr	caa Gln 380	tcg Ser	acc Thr	gtg Val	gcg Ala	cgc Arg	1152
cgc Arg 385	tgg Trp	cag Gln	cac His	ttc Phe 390	gcc Ala 390	ttc Phe	cgg Arg	gca Ala	gaa Glu 395	acg Thr 395	cgg Arg	atg Met	gag Glu	ttc Phe 400	tcg Ser 400	1200
ccg Pro	gtg Val	cac His	ttc Phe	cag Gln 405	cag Gln 405	agc Ser	gcg Ala	ggg Gly 410	ctg Leu 410	acc Thr	tgc Cys	tac Tyr	tac Tyr	aac Asn 415	agc Ser	1248
aaa Lys	aac Asn	tgg Trp	agc Ser 420	tac Tyr	tgc Cys	ttt Phe	gtg Val	gac Asp 425	tac Tyr	gag Glu	gag Glu	gga Gly	cag Gln 430	ggg Gly	aga Arg	1296
acc Thr	atc Ile	aaa Lys 435	gtt Val	atc Ile	cag Gln	ctc Leu	gac Asp 440	cac His	aac Asn	gtg Val	ccg Pro	tcg Ser	tgg Trp	ccg Pro	ctg Leu	1344
cac His	gag Glu 450	cag Gln	ccc Pro	att Ile	ccg Pro	gtg Val 455	ccg Pro	gaa Glu	cat His	gcg Ala	gag Glu	agc Ser	gtc Val	tgg Trp	ctg Leu	1392
cgg Arg 465	gtg Val	gac Asp	gtg Val	gat Asp 470	acg Thr 470	ctg Leu	gtc Val	tac Tyr	cgc Arg	tac Tyr 475	agc Ser	tac Tyr	tcg Ser	ttt Phe	gat Asp 480	1440
ggc Gly	gag Glu	acg Thr	tgg Trp	cac His 485	acc Thr	gtg Val	ccg Pro	gtg Val	acg Thr	tat Tyr 490	gag Glu	gcg Ala	tgg Trp	aag Lys 495	ctg Leu	1488
tcg Ser	gac Asp	gac Asp	tac Tyr 500	atc Ile	ggc Gly	ggg Gly	cgc Arg	ggc Gly	ttc Phe	ttc Phe	acc Thr	ggc Gly	gcg Ala	ttt Phe	gtg Val	1536
ggc Gly	ctg Leu	cac His 515	tgc Cys	gag Glu	gac Asp	atc Ile	agc Ser 520	ggc Gly	gac Asp	ggc Gly	tgc Cys	tac Tyr 525	gcg Ala	gac Asp	ttc Phe	1584
gac Asp	tac Tyr 530	ttc Phe	acc Thr	tac Tyr	gag Glu	ccg Pro 535	gtc Val	taa *								1611

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<210> 273
<211> 978
<212> DNA
<213> Escherichia coli
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<400> 273
ttg cat atg aaa aaa ata atc ttt gct ttt att ata tta ttt gtg ttt 48

225	230	235	240	
cag gta aaa gcg gca ttg ttg tca tct	cag gat tta tct gtt tat tct	768		
Gln Val Lys Ala Leu Leu Ser Ser	Gln Asp Leu Ser Val Tyr Ser			
245	250	255		
atg aat acc cca ggg ttt att ccc ggt att gat ttc tct gac cac ctg	816			
Met Asn Thr Pro Gly Phe Ile Pro Gly Ile Asp Phe Ser Asp His Leu				
260	265	270		
aat tat tgg caa cac gat att ccc gcc ata atg att act gac acc gct	864			
Asn Tyr Trp Gln His Asp Ile Pro Ala Ile Met Ile Thr Asp Thr Ala				
275	280	285		
ttt tat cgt aat aaa caa tac cac ttg ccc ggt gat acc gca gac aga	912			
Phe Tyr Arg Asn Lys Gln Tyr His Leu Pro Gly Asp Thr Ala Asp Arg				
290	295	300		
ttg aat tat cag aaa atg gct cag gta gtg gat ggt gtt ata act ttg	960			
Leu Asn Tyr Gln Lys Met Ala Gln Val Val Asp Gly Val Ile Thr Leu				
305	310	315	320	
tta tac aac agt aaa taa	978			
Leu Tyr Asn Ser Lys *				
325				
<210> 274				
<211> 963				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(963)				
<400> 274				
gtg atg atc aaa acg cgt ttt tct cgc tgg cta acg ttt ttt acg ttc	48			
Met Met Ile Lys Thr Arg Phe Ser Arg Trp Leu Thr Phe Phe Thr Phe				
1 5 10 15				
gcc gct gcc gtg gcg ctg gcg cta ccg gca aaa gcc aac acc tgg ccg	96			
Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro				
20 25 30				
ctg ccg cca gcg ggc agt cgt ctg gtt ggc gaa aac aaa ttt cat gtg	144			
Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val				
35 40 45				
gtg gaa aat gac ggt ggt tct ctg gaa gcc atc gcc aaa aaa tac aac	192			
Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn				
50 55 60				
gtc ggc ttt ctc gct ctg tta cag gct aac ccc ggc gtt gat cct tac	240			
Val Gly Phe Leu Ala Leu Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr				
65 70 75 80				

Gly Met Pro Val Asp Val Arg Arg His Gln Val Ser Pro Gln Thr Leu
 305 310 315 320

taa 963
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<210> 275
 <211> 1485
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1485)

<400> 275
 gtg gtc gca atc cat ctt ttg ccg gtt agt tac aat tct gcg aca tcc 48
 Met Val Ala Ile His Leu Leu Pro Val Ser Tyr Asn Ser Ala Thr Ser
 1 5 10 15
 acc gtg aat atc agt gct aga atc ata ccc ctg ttg att att cac caa 96
 Thr Val Asn Ile Ser Ala Arg Ile Ile Pro Leu Leu Ile Ile His Gln
 20 25 30
 aga tat aaa att cct atg cca aaa gtt cag gcc gac ggc ctg cca ttg 144
 Arg Tyr Lys Ile Pro Met Pro Lys Val Gln Ala Asp Gly Leu Pro Leu
 35 40 45
 ccc cag cga tac ggt gcg ata tta acc att gtg att ggt att tcg atg 192
 Pro Gln Arg Tyr Gly Ala Ile Leu Thr Ile Val Ile Gly Ile Ser Met
 50 55 60
 gcc gtc ctt gac ggc gca atc gcc aac gtc gcc ctg cca aca atc gcc 240
 Ala Val Leu Asp Gly Ala Ile Ala Asn Val Ala Leu Pro Thr Ile Ala
 65 70 75 80
 acg gac ctt cat gcc acg cca gcc agt tcc atc tgg gta gtg aac gcc 288
 Thr Asp Leu His Ala Thr Pro Ala Ser Ser Ile Trp Val Val Asn Ala
 85 90 95
 tat caa atc gcc att gtc atc tcc ctg ctc tcg ttt tcg ttt ctg ggc 336
 Tyr Gln Ile Ala Ile Val Ile Ser Leu Leu Ser Phe Ser Phe Leu Gly
 100 105 110
 gat atg ttt ggc tat cga cgt att tat aaa tgc ggt ctg gtc gtt ttt 384
 Asp Met Phe Gly Tyr Arg Arg Ile Tyr Lys Cys Gly Leu Val Val Phe
 115 120 125
 ctg ttg tct tca ctg ttc tgc gcc ctt tct gat tcg ctg caa atg ctc 432
 Leu Leu Ser Ser Leu Phe Cys Ala Leu Ser Asp Ser Leu Gln Met Leu
 130 135 140
 acc ctt gcg cgt gtc ata caa ggt ttc ggc ggt gca gcg ttg atg agc 480
 Thr Leu Ala Arg Val Ile Gln Gly Phe Gly Ala Ala Leu Met Ser
 145 150 155 160

290	295	300	
ccg atc gag ctg gaa aat gct gta cgt gga cgt gca gat aca ggc ttt			960
Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe			
305	310	315	320
ggc gtg atg acc gaa gag gaa ctg aag ctg gcc gta gcg gca gcg cgt			1008
Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg			
	325	330	335
aaa cgt ggt gaa aaa gtg gtg atg acc aac ggt gtc ttt gac atc ctg			1056
Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu			
	340	345	350
cac gcc ggg cac gtc tct tat ctg gca aat gcc cgc aag ctg ggt gac			1104
His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp			
	355	360	365
cgc ttg att gtt gcc gtc aac agc gat gcc tcc acc aaa cgg ctg aaa			1152
Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys			
	370	375	380
ggg gat tcc cgc ccg gta aac cca ctc gaa cag cgt atg att gtg ctg			1200
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu			
	385	390	400
ggc gca ctg gaa gcg gtc gac tgg gta gtg tcg ttt gaa gag gac acg			1248
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr			
	405	410	415
ccg cag cgc ttg atc gcc ggg atc ttg cca gat ctg ctg gtg aaa ggc			1296
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly			
	420	425	430
ggc gac tat aaa cca gaa gag att gcc ggg agt aaa gaa gtc tgg gcc			1344
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala			
	435	440	445
aac ggt ggc gaa gtg ttg gtg ctc aac ttt gaa gac ggt tgc tcg acg			1392
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr			
	450	455	460
acc aac atc atc aag aag atc caa cag gat aaa aaa ggc taa			1434
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly *			
465	470	475	

<210> 277
 <211> 2841
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2841)

cat	ctg	gca	tta	cag	gaa	ttg	ccg	ggc	cat	gtg	tcg	gag	gat	tgc	ttc	2784
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe	
		915					920					925				

acc	gca	gag	cgt	gaa	ctg	gtg	cgg	gca	agc	tgg	cag	aag	tgg	ctg	gtg	2832
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val	
	930					935					940					

gaa	gaa	tga														2841
Glu	Glu	*														
945																

<210> 278
 <211> 1302
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1302)

<400>	278																
atg	gct	cag	gaa	atc	gaa	tta	aag	ttt	att	gtt	aat	cac	agt	gcc	gtt	48	
Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val		
1				5					10					15			

gag	gcg	ttg	cgt	gac	cat	ctc	aat	acg	ctg	ggc	ggc	gag	cac	cat	gac	96
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp	
			20					25					30			

ccc	gtg	cag	ttg	ctg	aat	att	tac	tac	gaa	acg	ccg	gat	aac	tgg	ctg	144
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu	
		35					40					45				

cgt	ggg	cac	gat	atg	ggc	tta	cgt	att	cgt	ggc	gaa	aac	ggg	cgc	tat	192
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr	
	50					55					60					

gag	atg	acc	atg	aaa	gtt	gca	gga	aga	gtg	aca	ggc	ggc	tta	cat	cag	240
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln	
65					70				75						80	

cgc	ccg	gaa	tat	aac	gtg	gcg	ttg	agc	gaa	ccg	acg	ctc	gac	ctg	gcg	288
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala	
				85					90					95		

cag	tta	ccg	acg	gaa	gtc	tgg	ccg	aac	ggc	gaa	ttg	ccc	gcc	gat	ctc	336
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu	
		100						105					110			

gcc	tcc	cgc	gtg	cag	ccg	ctg	ttc	agc	acc	gat	ttt	tat	cgc	gaa	aaa	384
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys	
		115				120						125				

tgg	ctg	gtg	gcg	gtc	gat	ggg	agc	caa	att	gaa	atc	gcc	ctc	gac	cag	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln	
130						135					140					
ggg	gaa	gtg	aaa	gcg	ggt	gaa	ttt	gct	gaa	cct	atc	tgt	gag	ctg	gaa	480
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu	
145					150					155					160	
ctg	gaa	ctg	ctt	agc	ggc	gac	acg	cgc	gcg	gtg	ctg	aaa	ctg	gcg	aac	528
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn	
				165					170					175		
caa	ctg	gta	tcg	caa	acc	gga	tta	cgc	cag	ggc	agc	ctg	agc	aaa	gcg	576
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala	
			180					185					190			
gcg	cgt	ggc	tat	cat	ctg	gcg	cag	ggc	aat	ccg	gcg	cgt	gaa	atc	aaa	624
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys	
		195					200					205				
ccg	acc	acc	att	ttg	cat	gtt	gcg	gca	aaa	gcc	gat	gtg	gaa	cag	ggg	672
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly	
	210					215					220					
ctg	gaa	gcg	gcg	ctc	gag	ctg	gcg	tta	gcg	caa	tgg	cag	tat	cat	gaa	720
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu	
225					230					235					240	
gaa	ctg	tgg	gta	cgc	ggc	aac	gat	gcg	gcg	aaa	gaa	cag	gtg	ctg	gca	768
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala	
				245					250					255		
gcc	att	agc	ctg	gtc	cgt	cat	acg	ctg	atg	ctg	ttc	ggg	ggg	att	gtg	816
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val	
			260					265					270			
ccg	cgt	aaa	gcg	agc	act	cac	tta	cgt	gat	ctg	ctg	act	caa	tgc	gag	864
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu	
		275					280					285				
gcg	acc	att	gct	tct	gcg	gtg	tct	gcc	gtg	acg	gcg	gtc	tac	tct	acc	912
Ala	Thr	Ile	Ala	Ser	Ala	Val	Ser	Ala	Val	Thr	Ala	Val	Tyr	Ser	Thr	
	290					295					300					
gaa	acg	gca	atg	gcg	aag	ctg	gcg	ttg	acc	gaa	tgg	ttg	gta	agc	aaa	960
Glu	Thr	Ala	Met	Ala	Lys	Leu	Ala	Leu	Thr	Glu	Trp	Leu	Val	Ser	Lys	
305					310					315					320	
gca	tgg	cag	cca	ttt	tta	gat	gcc	aaa	gcg	cag	ggc	aaa	atc	agc	gac	1008
Ala	Trp	Gln	Pro	Phe	Leu	Asp	Ala	Lys	Ala	Gln	Gly	Lys	Ile	Ser	Asp	
				325				330						335		
tcc	ttc	aaa	cgc	ttt	gcc	gat	atc	cat	ctt	tcc	cgc	cat	gcc	gct	gaa	1056
Ser	Phe	Lys	Arg	Phe												

355	360	365	
ttg cca cgc ctg acg cgt gat att gac tca ata ctg ttg ctg gcg ggt			1152
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly			
370	375	380	
tac tat gat cct gtc gtc gcg caa gcc tgg ctg gag aac tgg cag ggg			1200
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly			
385	390	395	400
ctg cat cac gct att gcg acc ggg caa cgc atc gaa att gaa cat ttc			1248
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe			
405	410	415	
cgt aat gag gca aac aat cag gaa ccg ttc tgg ttg cac agc gga aaa			1296
Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys			
420	425	430	
cgt taa			1302
Arg *			

<210> 279
 <211> 624
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(624)

<400> 279	
gtg ctc aac aaa ctc tcc tta ctg ctg aaa gac gca ggt att tcg ctt	48
Met Leu Asn Lys Leu Ser Leu Leu Leu Lys Asp Ala Gly Ile Ser Leu	
1 5 10 15	
acc gat cac cag aaa aac cag ctt att gcc tac gtg aat atg ctg cat	96
Thr Asp His Gln Lys Asn Gln Leu Ile Ala Tyr Val Asn Met Leu His	
20 25 30	
aaa tgg aac aaa gcg tac aac ctg act tcg gtc cgc gat cct aat gag	144
Lys Trp Asn Lys Ala Tyr Asn Leu Thr Ser Val Arg Asp Pro Asn Glu	
35 40 45	
atg ctg gta cgc cat att ctc gat agc att gtg gtg gca ccg tat ctg	192
Met Leu Val Arg His Ile Leu Asp Ser Ile Val Val Ala Pro Tyr Leu	
50 55 60	
caa ggt gaa cgg ttt atc gat gtc ggc acc gga cca gga ctg cca ggc	240
Gln Gly Glu Arg Phe Ile Asp Val Gly Thr Gly Pro Gly Leu Pro Gly	
65 70 75 80	
att cca ctc tct atc gtg cgt cct gaa gcc cat ttc act ctg ttg gat	288
Ile Pro Leu Ser Ile Val Arg Pro Glu Ala His Phe Thr Leu Leu Asp	
85 90 95	

300

ctg cgt cgt ccg gaa atg act tat gaa aaa tta acc acg ctg acg ccg 1584
Leu Arg Arg Pro Glu Met Thr Tyr Glu Lys Leu Thr Thr Leu Thr Pro
515 520 525

ctc act cac ctt gag cag ctg caa aaa cac cag gga aat acc att gaa 336
 Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
 100 105 110

att cgt tac acc acg cat gaa caa ttc aaa caa caa acc gca gaa agt 384
 Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser
 115 120 125

cag gcg gta att cgc agc gga gaa tgt tct ccg tat gcg aat atc att 432
 Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile
 130 135 140

ctc tgt gct ggc gtg acg ttc tga 456
 Leu Cys Ala Gly Val Thr Phe *
 145 150

<210> 283
 <211> 1506
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1506)

<400> 283
 atg gaa gca tta ctt cag ctt aaa ggc atc gat aaa gcc ttc ccg ggc 48
 Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly
 1 5 10 15

gta aaa gcc ctc tcg ggc gca gcg tta aat gtc tat ccg ggc cgc gtg 96
 Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val
 20 25 30

atg gcg ctg gtg ggc gaa aac ggc gcg ggt aaa tcc acc atg atg aaa 144
 Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys
 35 40 45

gtg ctt act ggc atc tat act cgc gat gcc ggt acg ctt tta tgg ctg 192
 Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu
 50 55 60

ggg aaa gaa acg aca ttt acc ggg cca aaa tct tcc cag gaa gcc ggg 240
 Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly
 65 70 75 80

att ggg att atc cat cag gaa ctg aac ctg atc ccg cag ttg acc att 288
 Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile
 85 90 95

gcc gaa aac att ttc ctc ggt cgt gag ttt gtt aat cgc ttt ggc aaa 336
 Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys
 100 105 110

att gac tgg aaa acc atg tat gcc gaa gcg gat aaa ttg ctg gct aaa 384

340						345						350						
ctg	aca	gcg	ctg	cgc	tac	ttc	agc	cgc	gct	ggc	ggc	agt	ttg	aag	cat	1104		
Leu	Thr	Ala	Leu	Arg	Tyr	Phe	Ser	Arg	Ala	Gly	Gly	Ser	Leu	Lys	His			
355						360						365						
gcc	gat	gaa	cag	cag	gct	gtg	agt	gat	ttc	att	cgt	ctg	ttt	aat	gtg	1152		
Ala	Asp	Glu	Gln	Gln	Ala	Val	Ser	Asp	Phe	Ile	Arg	Leu	Phe	Asn	Val			
370						375						380						
aaa	act	ccg	tcg	atg	gaa	cag	gca	att	ggt	ctg	ctt	tcc	ggt	ggc	aat	1200		
Lys	Thr	Pro	Ser	Met	Glu	Gln	Ala	Ile	Gly	Leu	Leu	Ser	Gly	Gly	Asn			
385						390						395						400
cag	caa	aaa	gtg	gcg	att	gcc	cgc	ggt	ctg	atg	aca	cgc	ccc	aaa	gtg	1248		
Gln	Gln	Lys	Val	Ala	Ile	Ala	Arg	Gly	Leu	Met	Thr	Arg	Pro	Lys	Val			
405						410						415						
ttg	atc	ctt	gat	gaa	cct	acc	cgt	ggc	gta	gat	gtc	ggc	gcg	aaa	aaa	1296		
Leu	Ile	Leu	Asp	Glu	Pro	Thr	Arg	Gly	Val	Asp	Val	Gly	Ala	Lys	Lys			
420						425						430						
gag	atc	tat	caa	ctg	att	aac	cag	ttc	aaa	gcc	gat	ggc	ttg	agc	atc	1344		
Glu	Ile	Tyr	Gln	Leu	Ile	Asn	Gln	Phe	Lys	Ala	Asp	Gly	Leu	Ser	Ile			
435						440						445						
att	ctg	gtg	tca	tcg	gag	atg	cca	gaa	gta	tta	ggc	atg	agc	gat	cgc	1392		
Ile	Leu	Val	Ser	Ser	Glu	Met	Pro	Glu	Val	Leu	Gly	Met	Ser	Asp	Arg			
450						455						460						
atc	atc	gtc	atg	cat	gaa	ggg	cat	ctc	agc	ggg	gaa	ttt	act	cgt	gag	1440		
Ile	Ile	Val	Met	His	Glu	Gly	His	Leu	Ser	Gly	Glu	Phe	Thr	Arg	Glu			
465						470						475						480
cag	gcc	acc	cag	gaa	gtg	tta	atg	gct	gcc	gct	gtg	ggc	aag	ctt	aat	1488		
Gln	Ala	Thr	Gln	Glu	Val	Leu	Met	Ala	Ala	Ala	Val	Gly	Lys	Leu	Asn			
485						490						495						
cgc	gtg	aat	cag	gag	taa											1506		
Arg	Val	Asn	Gln	Glu	*													
500																		

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<210> 284
<211> 966
<212> DNA
<213> Escherichia coli
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<220>  
<221> CDS  
<222> (1) ... (966)
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<400> 284
atg aca acc cag act gtc tct ggt cgc cgt tat ttc acg aaa gcg tgg 48
Met Thr Thr Gln Thr Val Ser Gly Arg Arg Tyr Phe Thr Lys Ala Trp
1 5 10 15

ctg atg gag cag aaa tcg ctt atc gct ctg ctg gtg ctg atc gcg att	96
Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile	
20 25 30	
gtc tcg acg tta agc ccg aac ttt ttc acc atc aat aac tta ttc aat	144
Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn	
35 40 45	
att ctc cag caa acc tca gtg aac gcc att atg gcg gtc ggg atg acg	192
Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr	
50 55 60	
ctg gtg atc ctg acg tcg ggc atc gac tta tcg gta ggt tct ctg ttg	240
Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu	
65 70 75 80	
gcg ctg acc ggc gca gtt gct gca tct atc gtc ggc att gaa gtc aat	288
Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn	
85 90 95	
gcg ctg gtg gct gtc gct gct gct ctc gcg tta ggt gcc gca att ggt	336
Ala Leu Val Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly	
100 105 110	
gcg gta acc ggg gtg att gta gcg aaa ggt cgc gtc cag gcg ttt atc	384
Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile	
115 120 125	
gct acg ctg gtt atg atg ctt tta ctg cgc ggc gtg acc atg gtt tat	432
Ala Thr Leu Val Met Met Leu Leu Leu Arg Gly Val Thr Met Val Tyr	
130 135 140	
acc aac ggt agc cca gtg aat acc ggc ttt act gag aac gcc gat ctg	480
Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu	
145 150 155 160	
ttt ggc tgg ttt ggt att ggt cgt ccg ctg ggc gta ccg acg cca gtc	528
Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val	
165 170 175	
tgg atc atg ggg att gtc ttc ctc gcg gcc tgg tac atg ctg cat cac	576
Trp Ile Met Gly Ile Val Phe Leu Ala Ala Trp Tyr Met Leu His His	
180 185 190	
acg cgt ctg ggg cgt tac atc tac gcg ctg ggc ggc aac gaa gcg gca	624
Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala	
195 200 205	
acg cgt ctt tct ggt atc aac gtc aat aaa atc aaa atc atc gtc tat	672
Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr	
210 215 220	
tct ctt tgt ggt ctg ctg gca tcg ctg gcc ggg atc att gaa gtg gcg	720
Ser Leu Cys Gly Leu Leu Ala Ser Leu Ala Gly Ile Ile Glu Val Ala	
225 230 235 240	
cgt ctc tcc tcc gca caa ccc acg gcg ggg act ggc tat gag ctg gat	768

Arg	Leu	Ser	Ser	Ala	Gln	Pro	Thr	Ala	Gly	Thr	Gly	Tyr	Glu	Leu	Asp	
				245					250					255		
gct	att	gct	gcg	gtg	gtt	ctg	ggc	ggt	acg	agt	ctg	gcg	ggc	gga	aaa	816
Ala	Ile	Ala	Ala	Val	Val	Leu	Gly	Gly	Thr	Ser	Leu	Ala	Gly	Gly	Lys	
			260				265					270				
ggt	cgc	att	gtt	ggg	acg	ttg	atc	ggc	gca	tta	att	ctt	ggc	ttc	ctt	864
Gly	Arg	Ile	Val	Gly	Thr	Leu	Ile	Gly	Ala	Leu	Ile	Leu	Gly	Phe	Leu	
		275				280						285				
aat	aat	gga	ttg	aat	ttg	tta	ggt	gtt	tcc	tcc	tat	tac	cag	atg	atc	912
Asn	Asn	Gly	Leu	Asn	Leu	Leu	Gly	Val	Ser	Ser	Tyr	Tyr	Gln	Met	Ile	
	290					295					300					
gtc	aaa	gcg	gtg	gtg	att	ttg	ctg	gcg	gtg	ctg	gta	gac	aac	aaa	aag	960
Val	Lys	Ala	Val	Val	Ile	Leu	Leu	Ala	Val	Leu	Val	Asp	Asn	Lys	Lys	
305					310					315					320	
cag	taa															966
Gln	*															

<210> 285
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(891)

<400>	285															
atg	aac	atg	aaa	aaa	ctg	gct	acc	ctg	gtt	tcc	gct	gtt	gcg	cta	agc	48
Met	Asn	Met	Lys	Lys	Leu	Ala	Thr	Leu	Val	Ser	Ala	Val	Ala	Leu	Ser	
1				5					10					15		
gcc	acc	gtc	agt	gcg	aat	gcg	atg	gca	aaa	gac	acc	atc	gcg	ctg	gtg	96
Ala	Thr	Val	Ser	Ala	Asn	Ala	Met	Ala	Lys	Asp	Thr	Ile	Ala	Leu	Val	
			20				25						30			
gtc	tcc	acg	ctt	aac	aac	ccg	ttc	ttt	gta	tcg	ctg	aaa	gat	ggc	gcg	144
Val	Ser	Thr	Leu	Asn	Asn	Pro	Phe	Phe	Val	Ser	Leu	Lys	Asp	Gly	Ala	
			35				40					45				
cag	aaa	gag	gcg	gat	aaa	ctt	ggc	tat	aac	ctg	gtg	gtg	ctg	gac	tcc	192
Gln	Lys	Glu	Ala	Asp	Lys	Leu	Gly	Tyr	Asn	Leu	Val	Val	Leu	Asp	Ser	
	50					55					60					
cag	aac	aac	ccg	gcg	aaa	gag	ctg	gcg	aac	gtg	cag	gac	tta	acc	gtt	240
Gln	Asn	Asn	Pro	Ala	Lys	Glu	Leu	Ala	Asn	Val	Gln	Asp	Leu	Thr	Val	
	65				70				75					80		
cgc	ggc	aca	aaa	att	ctg	ctg	att	aac	ccg	acc	gac	tcc	gac	gca	gtg	288
Arg	Gly	Thr	Lys	Ile	Leu	Leu	Ile	Asn	Pro	Thr	Asp	Ser	Asp	Ala	Val	
				85					90					95		

ggt Gly	aat Asn	gct Ala	gtg Val	aag Lys	atg Met	gct Ala	aac Asn	cag Gln	gcg Ala	aac Asn	atc Ile	ccg Pro	gtt Val	atc Ile	act Thr	336
100110																
ctt Leu	gac Asp	cgc Arg	cag Gln	gca Ala	acg Thr	aaa Lys	ggt Gly	gaa Glu	gtg Val	gtg Val	agc Ser	cac His	att Ile	gct Ala	tct Ser	384
115120125																
gat Asp	aac Asn	gta Val	ctg Leu	ggc Gly	ggc Gly	aaa Lys	atc Ile	gct Ala	ggt Gly	gat Asp	tac Tyr	atc Ile	gcg Ala	aag Lys	aaa Lys	432
130135140																
gcg Ala	ggt Gly	gaa Glu	ggt Gly	gcc Ala	aaa Lys	gtt Val	atc Ile	gag Glu	ctg Leu	caa Gln	ggc Gly	att Ile	gct Ala	ggt Gly	aca Thr	480
145150155160																
tcc Ser	gca Ala	gcc Ala	cgt Arg	gaa Glu	cgt Arg	ggc Gly	gaa Glu	ggc Gly	ttc Phe	cag Gln	cag Gln	gcc Ala	gtt Val	gct Ala	gct Ala	528
165170175																
cac His	aag Lys	ttt Phe	aat Asn	gtt Val	ctt Leu	gcc Ala	agc Ser	cag Gln	cca Pro	gca Ala	gat Asp	ttt Phe	gat Asp	cgc Arg	att Ile	576
180185190																
aaa Lys	ggt Gly	ttg Leu	aac Asn	gta Val	atg Met	cag Gln	aac Asn	ctg Leu	ttg Leu	acc Thr	gct Ala	cat His	ccg Pro	gat Asp	gtt Val	624
195200205																
cag Gln	gct Ala	gta Val	ttc Phe	gcg Ala	cag Gln	aat Asn	gat Asp	gaa Glu	atg Met	gcg Ala	ctg Leu	ggc Gly	gcg Ala	ctg Leu	cgc Arg	672
210215220																
gca Ala	ctg Leu	caa Gln	act Thr	gcc Ala	ggc Gly	aaa Lys	tcg Ser	gat Asp	gtg Val	atg Met	gtc Val	gtc Val	gga Gly	ttt Phe	gac Asp	720
225230235240																
ggt Gly	aca Thr	ccg Pro	gat Asp	ggc Gly	gaa Glu	aaa Lys	gcg Ala	gtg Val	aat Asn	gat Asp	ggc Gly	aaa Lys	cta Leu	gca Ala	gcg Ala	768
245250255																
act Thr	atc Ile	gct Ala	cag Gln	cta Leu	ccc Pro	gat Asp	cag Gln	att Ile	ggc Gly	gcg Ala	aaa Lys	ggc Gly	gtc Val	gaa Glu	acc Thr	816
260265270																
gca Ala	gat Asp	aaa Lys	gtg Val	ctg Leu	aaa Lys	ggc Gly	gag Glu	aaa Lys	gtt Val	cag Gln	gct Ala	aag Lys	tat Tyr	ccg Pro	gtt Val	864
275280285																
gat Asp	ctg Leu	aaa Lys	ctg Leu	gtt Val	gtt Val	aag Lys	cag Gln	tag *								891
290295																

<210>	286
<211>	930
<212>	DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(930)

<400> 286

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Met	Gln	Asn	Ala	Gly	Ser	Leu	Val	Val	Leu	Gly	Ser	Ile	Asn	Ala	Asp	
1				5					10					15		
cac	att	ctt	aat	ctt	caa	tct	ttt	cct	act	cca	ggc	gaa	acc	gta	acc	96
His	Ile	Leu	Asn	Leu	Gln	Ser	Phe	Pro	Thr	Pro	Gly	Glu	Thr	Val	Thr	
			20					25					30			
ggt	aac	cac	tat	cag	gtt	gca	ttt	ggc	ggc	aaa	ggc	gcg	aat	cag	gct	144
Gly	Asn	His	Tyr	Gln	Val	Ala	Phe	Gly	Gly	Lys	Gly	Ala	Asn	Gln	Ala	
		35					40					45				
gtg	gct	gct	ggg	cgt	agc	ggt	gcg	aat	atc	gcg	ttt	att	gcc	tgt	acg	192
Val	Ala	Ala	Gly	Arg	Ser	Gly	Ala	Asn	Ile	Ala	Phe	Ile	Ala	Cys	Thr	
	50					55					60					
ggt	gat	gac	agc	att	ggt	gag	agc	gtt	cgc	cag	cag	ctc	gcc	act	gat	240
Gly	Asp	Asp	Ser	Ile	Gly	Glu	Ser	Val	Arg	Gln	Gln	Leu	Ala	Thr	Asp	
65					70				75					80		
aac	att	gat	att	act	ccg	gtc	agc	gtg	atc	aaa	ggc	gaa	tca	aca	ggt	288
Asn	Ile	Asp	Ile	Thr	Pro	Val	Ser	Val	Ile	Lys	Gly	Glu	Ser	Thr	Gly	
				85					90					95		
gtg	gcg	ctg	att	ttt	gtt	aat	ggc	gaa	ggt	gag	aat	gtc	atc	ggt	att	336
Val	Ala	Leu	Ile	Phe	Val	Asn	Gly	Glu	Gly	Glu	Asn	Val	Ile	Gly	Ile	
			100					105					110			
cat	gcc	ggc	gct	aat	gct	gcc	ctt	tcc	ccg	gcg	ctg	gtg	gaa	gcg	caa	384
His	Ala	Gly	Ala	Asn	Ala	Ala	Leu	Ser	Pro	Ala	Leu	Val	Glu	Ala	Gln	
		115					120						125			
cgt	gag	cgt	att	gcc	aac	gcg	tca	gca	tta	tta	atg	cag	ctg	gaa	tca	432
Arg	Glu	Arg	Ile	Ala	Asn	Ala	Ser	Ala	Leu	Leu	Met	Gln	Leu	Glu	Ser	
	130					135					140					
cca	ctc	gaa	agt	gtg	atg	gca	gcg	gcg	aaa	atc	gcc	cat	caa	aat	aag	480
Pro	Leu	Glu	Ser	Val	Met	Ala	Ala	Ala	Lys	Ile	Ala	His	Gln	Asn	Lys	
	145				150					155					160	
act	atc	gtt	gcg	ctt	aac	ccg	gct	ccg	gct	cgc	gaa	ctt	cct	gac	gaa	528
Thr	Ile	Val	Ala	Leu	Asn	Pro	Ala	Pro	Ala	Arg	Glu	Leu	Pro	Asp	Glu	
				165					170					175		
ctg	ctg	gcg	ctg	gtg	gac	att	att	acg	cca	aac	gaa	acg	gaa	gca	gaa	576
Leu	Leu	Ala	Leu	Val	Asp	Ile	Ile	Thr	Pro	Asn	Glu	Thr	Glu	Ala	Glu	
			180					185					190			
aag	ctc	acc	ggt	att	cgt	gtt	gaa	aat	gat	gaa	gat	gca	gcg	aag	gcg	624
Lys	Leu	Thr	Gly	Ile	Arg	Val	Glu	Asn	Asp	Glu	Asp	Ala	Ala	Lys	Ala	

<400> 289

Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
1 5 10 15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
20 25 30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
35 40 45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
50 55 60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65 70 75 80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
85 90 95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
100 105 110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
115 120 125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
130 135 140

<210> 290

<211> 59

<212> PRT

<213> Escherichia coli

<400> 290

Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1 5 10 15
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
20 25 30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
35 40 45
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
50 55

<210> 291

<211> 167

<212> PRT

<213> Escherichia coli

<400> 291

Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
1 5 10 15
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
20 25 30
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
35 40 45
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
50 55 60
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65 70 75 80
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
85 90 95
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
100 105 110

Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160
 Val Glu Glu Ile Leu Gly Lys
 165

<210> 292
 <211> 117
 <212> PRT
 <213> Escherichia coli

<400> 292
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
 35 40 45
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50 55 60
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
 65 70 75 80
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
 85 90 95
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
 100 105 110
 Ala Gly Leu Gln Phe
 115

<210> 293
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 293
 Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
 1 5 10 15
 Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
 20 25 30
 Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
 35 40 45
 Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
 50 55 60
 Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
 65 70 75 80
 Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
 85 90 95
 Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
 100 105 110
 Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
 115 120 125
 Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val

130 135 140
 Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
 145 150 155 160
 Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
 165 170 175
 Lys

<210> 294
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 294
 Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
 1 5 10 15
 Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
 20 25 30
 Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
 35 40 45
 Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
 50 55 60
 Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
 65 70 75 80
 Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
 85 90 95
 Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
 100 105 110
 Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
 115 120 125
 Val Ala
 130

<210> 295
 <211> 101
 <212> PRT
 <213> Escherichia coli

<400> 295
 Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1 5 10 15
 Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
 20 25 30
 Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
 35 40 45
 Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
 50 55 60
 Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
 65 70 75 80
 Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
 85 90 95
 Lys Lys Ala Ser Trp
 100

<210> 296
 <211> 179
 <212> PRT
 <213> Escherichia coli

<400> 296
 Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1 5 10 15
 Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
 20 25 30
 Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
 35 40 45
 Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
 50 55 60
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110
 Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125
 Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
 130 135 140
 Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
 145 150 155 160
 Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
 165 170 175
 Phe Arg Lys

<210> 297
 <211> 104
 <212> PRT
 <213> Escherichia coli

<400> 297
 Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1 5 10 15
 Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
 20 25 30
 Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 298
 <211> 123
 <212> PRT

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

Met	Ile	Gln	Glu	Gln	Thr	Met	Leu	Asn	Val	Ala	Asp	Asn	Ser	Gly	Ala
1				5					10					15	
Arg	Arg	Val	Met	Cys	Ile	Lys	Val	Leu	Gly	Gly	Ser	His	Arg	Arg	Tyr
			20					25					30		
Ala	Gly	Val	Gly	Asp	Ile	Ile	Lys	Ile	Thr	Ile	Lys	Glu	Ala	Ile	Pro
			35				40					45			
Arg	Gly	Lys	Val	Lys	Lys	Gly	Asp	Val	Leu	Lys	Ala	Val	Val	Val	Arg
			50			55					60				
Thr	Lys	Lys	Gly	Val	Arg	Arg	Pro	Asp	Gly	Ser	Val	Ile	Arg	Phe	Asp
65					70					75				80	
Gly	Asn	Ala	Cys	Val	Leu	Leu	Asn	Asn	Asn	Ser	Glu	Gln	Pro	Ile	Gly
				85					90					95	
Thr	Arg	Ile	Phe	Gly	Pro	Val	Thr	Arg	Glu	Leu	Arg	Ser	Glu	Lys	Phe
			100					105					110		
Met	Lys	Ile	Ile	Ser	Leu	Ala	Pro	Glu	Val	Leu					
			115				120								

<211> 485

<212> PRT

<213> Escherichia coli

Met 1	Gly	Ile	Tyr	Phe 5	Thr	Asn	Ser	Asp	Asp 10	Gln	Ile	Tyr	Phe	Lys 15	Arg
Ser	Glu	Gly	Met 20	Ser	Asp	Ile	Asn	His 25	Ala	Gly	Ser	Asp	Leu 30	Ile	Phe
Glu	Leu	Glu	Asp 35	Arg	Pro	Pro	Phe 40	His	Gln	Ala	Leu	Val 45	Gly	Ala	Ile
Thr	His 50	Leu	Leu	Ala	Ile	Phe 55	Val	Pro	Met	Val	Thr 60	Pro	Ala	Leu	Ile
Val 65	Gly	Ala	Ala	Leu	Gln 70	Leu	Ser	Ala	Glu	Thr 75	Ala	Tyr	Leu 80	Val	
Ser	Met	Ala	Met 85	Ile	Ala	Ser	Gly	Ile	Gly 90	Thr	Trp	Leu	Gln 95	Val	Asn
Arg	Tyr	Gly	Ile 100	Val	Gly	Ser	Gly	Leu 105	Leu	Ser	Ile	Gln	Ser 110	Val	Asn
Phe	Ser	Phe 115	Val	Thr	Val	Met	Ile 120	Ala	Leu	Gly	Ser	Ser 125	Met	Lys	Ser
Asp	Gly 130	Phe	His	Glu	Glu	Leu 135	Ile	Met	Ser	Ser	Leu 140	Leu	Gly	Val	Ser
Phe 145	Val	Gly	Ala	Phe	Leu 150	Val	Val	Gly	Ser	Ser 155	Phe	Ile	Leu	Pro 160	Tyr
Leu	Arg	Arg	Val 165	Ile	Thr	Pro	Thr	Val	Ser 170	Gly	Ile	Val	Val	Leu 175	Met
Ile	Gly	Leu	Ser 180	Leu	Ile	Lys	Val	Gly 185	Ile	Ile	Asp	Phe	Gly 190	Gly	Gly
Phe	Ala	Ala 195	Lys	Ser	Ser	Gly	Thr 200	Phe	Gly	Asn	Tyr 205	Glu	His	Leu	Gly
Val	Gly 210	Leu	Leu	Val	Leu	Ile 215	Val	Val	Ile	Gly	Phe 220	Asn	Cys	Cys	Arg
Ser 225	Pro	Leu	Leu	Arg	Met 230	Gly	Gly	Ile	Ala	Ile 235	Gly	Leu	Cys	Val	Gly 240

	130					135					140				
His 145	Pro	Gln	Ser	Val	Asp 150	Ala	Leu	Phe	Glu	Ala 155	Ala	Ser	His	Ile	Asn 160
Met	Arg	Met	Ile	Ala 165	Gly	Lys	Val	Met	Met 170	Asp	Arg	Asn	Ala	Pro	Asp 175
Tyr	Leu	Leu	Asp	Thr 180	Ala	Glu	Ser	Ser	Tyr 185	His	Gln	Ser	Lys	Glu	Leu 190
Ile	Glu	Arg	Trp	His 195	Lys	Asn	Gly	Arg	Leu 200	Leu	Tyr	Ala	Ile	Thr	Pro 205
Arg	Phe	Ala	Pro	Thr 210	Ser	Ser	Pro	Glu	Gln 215	Met	Ala	Met	Ala	Gln	Arg 220
Leu 225	Lys	Glu	Glu	Tyr 230	Pro	Asp	Thr	Trp	Val 235	His	Thr	His	Leu	Cys	Glu 240
Asn	Lys	Asp	Glu	Ile 245	Ala	Trp	Val	Lys	Ser 250	Leu	Tyr	Pro	Asp	His	Asp 255
Gly	Tyr	Leu	Asp	Val 260	Tyr	His	Gln	Tyr	Gly 265	Leu	Thr	Gly	Lys	Asn	Cys 270
Val	Phe	Ala	His	Cys 275	Val	His	Leu	Glu	Glu 280	Lys	Glu	Trp	Asp	Arg	Leu 285
Ser	Glu	Thr	Lys	Ser 290	Ser	Ile	Ala	Phe	Cys 295	Pro	Thr	Ser	Asn	Leu	Tyr 300
Leu 305	Gly	Ser	Gly	Leu 310	Phe	Asn	Leu	Lys	Lys 315	Ala	Trp	Gln	Lys	Lys	Val 320
Lys	Val	Gly	Met	Gly 325	Thr	Asp	Ile	Gly	Ala 330	Gly	Thr	Thr	Phe	Asn	Met 335
Leu	Gln	Thr	Leu	Asn 340	Glu	Ala	Tyr	Lys	Val 345	Leu	Gln	Leu	Gln	Gly	Tyr 350
Arg	Leu	Ser	Ala	Tyr 355	Glu	Ala	Phe	Tyr	Leu 360	Ala	Thr	Leu	Gly	Gly	Ala 365
Lys	Ser	Leu	Gly	Leu 370	Asp	Asp	Leu	Ile	Gly 375	Asn	Phe	Leu	Pro	Gly	Lys 380
Glu 385	Ala	Asp	Phe	Val 390	Val	Met	Glu	Pro	Thr 395	Ala	Thr	Pro	Leu	Gln	Gln 400
Leu	Arg	Tyr	Asp	Asn 405	Ser	Val	Ser	Leu	Val 410	Asp	Lys	Leu	Phe	Val	Met 415
Met	Thr	Leu	Gly	Asp 420	Asp	Arg	Ser	Ile	Tyr 425	Arg	Thr	Tyr	Val	Asp	Gly 430
Arg	Leu	Val	Tyr	Glu 435	Arg	Asn									

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<210> 301
<211> 189
<212> PRT
<213> Escherichia coli
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<400> 301															
Met	Ser	Gly	Asp	Ile	Leu	Gln	Thr	Pro	Asp	Ala	Pro	Lys	Pro	Gln	Gly
1				5					10					15	
Ala	Leu	Asp	Asn	Tyr	Phe	Lys	Ile	Thr	Ala	Arg	Gly	Ser	Thr	Val	Arg
			20					25					30		
Gln	Glu	Val	Leu	Ala	Gly	Leu	Thr	Thr	Phe	Leu	Ala	Met	Val	Tyr	Ser
		35					40					45			
Val	Ile	Val	Val	Pro	Gly	Met	Leu	Gly	Lys	Ala	Gly	Phe	Pro	Pro	Ala
	50					55					60				
Ala	Val	Phe	Val	Ala	Thr	Cys	Leu	Val	Ala	Gly	Phe	Gly	Ser	Leu	Leu
65					70					75					80

Met	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Met	Ala	Ile	Gly	Cys	Ala	Ile	Ser
				85					90					95	
Leu	Thr	Ala	Phe	Thr	Ala	Phe	Ser	Leu	Val	Leu	Gly	Gln	Gln	Ile	Ser
			100					105					110		
Val	Pro	Val	Ala	Leu	Gly	Ala	Val	Phe	Leu	Met	Gly	Val	Ile	Phe	Thr
		115					120					125			
Ala	Ile	Ser	Val	Thr	Gly	Val	Arg	Thr	Trp	Ile	Leu	Arg	Asn	Leu	Pro
	130					135					140				
Met	Gly	Ile	Ala	His	Gly	Thr	Gly	Ile	Gly	Ile	Gly	Leu	Phe	Leu	Leu
145					150					155					160
Leu	Ile	Ala	Ala	Asn	Gly	Val	Gly	Met	Val	Ile	Lys	Asn	Pro	Ile	Glu
				165				170						175	
Gly	Leu	Gln	Trp	Arg	Ser	Val	Arg	Leu	Pro	Pro	Ser	Arg			
			180					185							

<210> 302
 <211> 276
 <212> PRT
 <213> Escherichia coli

<400> 302

Met	Ala	Leu	Gly	Ala	Phe	Thr	Ser	Phe	Pro	Val	Met	Met	Ser	Leu	Leu
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Gly	Leu	Ala	Val	Ile	Phe	Gly	Leu	Glu	Lys	Cys	Arg	Val	Pro	Gly	Gly
			20					25					30		
Ile	Leu	Leu	Val	Ile	Ile	Ala	Ile	Ser	Ile	Ile	Gly	Leu	Ile	Phe	Asp
		35					40					45			
Pro	Ala	Val	Lys	Tyr	His	Gly	Leu	Val	Ala	Met	Pro	Ser	Leu	Thr	Gly
	50					55				60					
Glu	Asp	Gly	Lys	Ser	Leu	Ile	Phe	Ser	Leu	Asp	Ile	Met	Gly	Ala	Leu
65					70				75						80
Gln	Pro	Thr	Val	Leu	Pro	Ser	Val	Leu	Ala	Leu	Val	Met	Thr	Ala	Val
				85				90						95	
Phe	Asp	Ala	Thr	Gly	Thr	Ile	Arg	Ala	Val	Ala	Gly	Gln	Ala	Asn	Leu
		100					105						110		
Leu	Asp	Lys	Asp	Asn	Gln	Ile	Ile	Asn	Gly	Gly	Lys	Ala	Leu	Thr	Ser
	115					120						125			
Asp	Ser	Val	Ser	Ser	Ile	Phe	Ser	Gly	Leu	Val	Gly	Ala	Ala	Pro	Ala
	130					135					140				
Ala	Val	Tyr	Ile	Glu	Ser	Ala	Ala	Gly	Thr	Ala	Ala	Gly	Gly	Lys	Thr
145					150				155						160
Gly	Leu	Thr	Ala	Thr	Val	Val	Gly	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Phe
				165				170						175	
Leu	Ser	Pro	Leu	Ser	Phe	Leu	Ile	Pro	Gly	Tyr	Ala	Thr	Ala	Pro	Ala
		180						185					190		
Leu	Met	Tyr	Val	Gly	Leu	Leu	Met	Leu	Ser	Asn	Val	Ser	Lys	Leu	Asp
	195					200						205			
Phe	Asn	Asp	Phe	Ile	Asp	Ala	Met	Ala	Gly	Leu	Val	Cys	Ala	Val	Phe
	210					215					220				
Ile	Val	Leu	Thr	Cys	Asn	Ile	Val	Thr	Gly	Ile	Met	Leu	Gly	Phe	Val
225					230				235						240
Thr	Leu	Val	Val	Gly	Arg	Val	Phe	Ala	Arg	Glu	Trp	Gln	Lys	Leu	Asn
				245				250						255	
Ile	Gly	Thr	Val	Ile	Ile	Thr	Ala	Ala	Leu	Val	Ala	Phe	Tyr	Ala	Gly
			260					265					270		
Gly	Trp	Ala	Ile												

<210> 303
 <211> 466
 <212> PRT
 <213> Escherichia coli

<400> 303

Met	Asn	Ser	Glu	Gly	Gly	Lys	Pro	Gly	Asn	Val	Leu	Thr	Val	Asn	Gly
1				5				10						15	
Asn	Tyr	Thr	Gly	Asn	Asn	Gly	Leu	Met	Thr	Phe	Asn	Ala	Thr	Leu	Gly
			20					25					30		
Gly	Asp	Asn	Ser	Pro	Thr	Asp	Lys	Met	Asn	Val	Lys	Gly	Asp	Thr	Gln
		35					40					45			
Gly	Asn	Thr	Arg	Val	Arg	Val	Asp	Asn	Ile	Gly	Gly	Val	Gly	Ala	Gln
		50				55					60				
Thr	Val	Asn	Gly	Ile	Glu	Leu	Ile	Glu	Val	Gly	Gly	Asn	Ser	Ala	Gly
65				70					75						80
Asn	Phe	Ala	Leu	Thr	Gly	Thr	Val	Glu	Ala	Gly	Ala	Tyr	Val	Tyr	
			85					90					95		
Thr	Leu	Ala	Lys	Gly	Lys	Gly	Asn	Asp	Glu	Lys	Asn	Trp	Tyr	Leu	Thr
			100					105					110		
Ser	Lys	Trp	Asp	Gly	Val	Thr	Pro	Ala	Asp	Thr	Pro	Asp	Pro	Ile	Asn
		115					120					125			
Asn	Pro	Pro	Val	Val	Asp	Pro	Glu	Gly	Pro	Ser	Val	Tyr	Arg	Pro	Glu
		130				135					140				
Ala	Gly	Ser	Tyr	Ile	Ser	Asn	Ile	Ala	Ala	Ala	Asn	Ser	Leu	Phe	Ser
145				150					155						160
His	Arg	Leu	His	Asp	Arg	Leu	Gly	Glu	Pro	Gln	Tyr	Thr	Asp	Ser	Leu
			165					170					175		
His	Ser	Gln	Gly	Ser	Ala	Ser	Ser	Met	Trp	Met	Arg	His	Val	Gly	Gly
			180					185					190		
His	Glu	Arg	Ser	Arg	Ala	Gly	Asp	Gly	Gln	Leu	Asn	Thr	Gln	Ala	Asn
		195					200					205			
Arg	Tyr	Val	Leu	Gln	Leu	Gly	Gly	Asp	Leu	Ala	Gln	Trp	Ser	Ser	Asn
	210					215					220				
Ala	Gln	Asp	Arg	Trp	His	Leu	Gly	Val	Met	Ala	Gly	Tyr	Ala	Asn	Gln
225				230					235						240
His	Ser	Asn	Thr	Gln	Ser	Asn	Arg	Val	Gly	Tyr	Lys	Ser	Asp	Gly	Arg
			245					250					255		
Ile	Ser	Gly	Tyr	Ser	Ala	Gly	Leu	Tyr	Ala	Thr	Trp	Tyr	Gln	Asn	Asp
		260						265					270		
Ala	Asn	Lys	Thr	Gly	Ala	Tyr	Val	Asp	Ser	Trp	Ala	Leu	Tyr	Asn	Trp
		275					280					285			
Phe	Asp	Asn	Ser	Val	Ser	Ser	Asp	Asn	Arg	Ser	Ala	Asp	Asp	Tyr	Asp
	290					295					300				
Ser	Arg	Gly	Val	Thr	Ala	Ser	Val	Glu	Gly	Gly	Tyr	Thr	Phe	Glu	Ala
305					310					315					320
Gly	Thr	Phe	Ser	Gly	Ser	Glu	Gly	Thr	Leu	Asn	Thr	Trp	Tyr	Val	Gln
			325					330						335	
Pro	Gln	Ala	Gln	Ile	Thr	Trp	Met	Gly	Val	Lys	Asp	Ser	Asp	His	Thr
		340						345					350		
Arg	Lys	Asp	Gly	Thr	Arg	Ile	Glu	Thr	Glu	Gly	Asp	Gly	Asn	Val	Gln
		355				360						365			
Thr	Arg	Leu	Gly	Val	Lys	Thr	Tyr	Leu	Asn	Ser	His	His	Gln	Arg	Asp
	370					375					380				

Asp Gly Lys Gln Arg Glu Phe Gln Pro Tyr Ile Glu Ala Asn Trp Ile
 385 390 395 400
 Asn Asn Ser Lys Val Tyr Ala Val Lys Met Asn Gly Gln Thr Val Gly
 405 410 415
 Arg Glu Gly Ala Arg Asn Leu Gly Glu Val Arg Thr Gly Val Glu Ala
 420 425 430
 Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
 435 440 445
 Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
 450 455 460
 Ser Trp
 465

<210> 304
 <211> 1325
 <212> PRT
 <213> Escherichia coli

<400> 304
 Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
 1 5 10 15
 Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
 20 25 30
 Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
 35 40 45
 Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
 50 55 60
 Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
 65 70 75 80
 Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
 85 90 95
 Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly
 100 105 110
 Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp
 115 120 125
 Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln
 130 135 140
 Ser Gly Thr Gly Thr Leu Asn Ile Lys Gln Lys Gly His Val Asp Gly
 145 150 155 160
 Gly Tyr Leu Arg Leu Gly Ser Ser Thr Gly Gly Val Gly Thr Val Asn
 165 170 175
 Val Glu Gly Glu Asp Ser Val Leu Thr Thr Glu Leu Phe Glu Ile Gly
 180 185 190
 Ser Tyr Gly Thr Gly Ser Leu Asn Ile Thr Asp Lys Gly Tyr Val Thr
 195 200 205
 Ser Ser Ile Val Ala Ile Leu Gly Tyr Gln Ala Gly Ser Asn Gly Gln
 210 215 220
 Val Val Val Glu Lys Gly Gly Glu Trp Leu Ile Lys Asn Asn Asp Ser
 225 230 235 240
 Ser Ile Glu Phe Gln Ile Gly Asn Gln Gly Thr Gly Glu Ala Thr Ile
 245 250 255
 Arg Glu Gly Gly Leu Val Thr Ala Glu Asn Thr Ile Ile Gly Gly Asn
 260 265 270
 Ala Thr Gly Ile Gly Thr Leu Asn Val Gln Asp Gln Asp Ser Val Ile
 275 280 285
 Thr Val Arg Arg Leu Tyr Asn Gly Tyr Phe Gly Asn Gly Thr Val Asn

Asp	Ile	Leu	Ala	Ser	Thr	Asn	Ser	Ala	Gly	Asp	Tyr	Thr	Leu	Thr	Asn
	755						760					765			
Ala	Leu	Lys	Gly	Asp	Gly	Leu	Met	Arg	Val	Gln	Leu	Ser	Ser	Ser	Asp
	770					775					780				
Lys	Met	Phe	Gly	Phe	Thr	His	Ala	Thr	Gly	Thr	Glu	Phe	Ala	Gly	Val
	785				790					795					800
Ala	Gln	Leu	Lys	Asp	Ser	Thr	Phe	Thr	Leu	Glu	Arg	Asp	Asn	Thr	Ala
			805						810					815	
Ala	Leu	Thr	His	Ala	Met	Leu	Gln	Ser	Asp	Ser	Glu	Asn	Thr	Thr	Ser
			820					825					830		
Val	Lys	Val	Gly	Glu	Gln	Ser	Ile	Gly	Gly	Leu	Ala	Met	Asn	Gly	Gly
	835						840					845			
Thr	Ile	Ile	Phe	Asp	Thr	Asp	Ile	Pro	Ala	Ala	Thr	Leu	Ala	Glu	Gly
	850					855					860				
Tyr	Ile	Ser	Val	Asp	Thr	Leu	Val	Val	Gly	Ala	Gly	Asp	Tyr	Thr	Trp
	865				870					875					880
Lys	Gly	Arg	Asn	Tyr	Gln	Val	Asn	Gly	Thr	Gly	Asp	Val	Leu	Ile	Asp
			885						890					895	
Val	Pro	Lys	Pro	Trp	Asn	Asp	Pro	Met	Ala	Asn	Asn	Pro	Leu	Thr	Thr
			900					905					910		
Leu	Asn	Leu	Leu	Glu	His	Asp	Asp	Ser	His	Val	Gly	Val	Gln	Leu	Val
	915						920					925			
Lys	Ala	Gln	Thr	Val	Ile	Gly	Ser	Gly	Gly	Ser	Leu	Thr	Leu	Arg	Asp
	930					935					940				
Leu	Gln	Gly	Asp	Glu	Val	Glu	Ala	Asp	Lys	Thr	Leu	His	Ile	Ala	Gln
	945				950					955					960
Asn	Gly	Thr	Val	Val	Ala	Glu	Gly	Asp	Tyr	Gly	Phe	Arg	Leu	Thr	Thr
			965						970					975	
Ala	Pro	Gly	Asn	Gly	Leu	Tyr	Val	Asn	Tyr	Gly	Leu	Lys	Ala	Leu	Asn
			980					985					990		
Ile	His	Gly	Gly	Gln	Lys	Leu	Thr	Leu	Ala	Glu	His	Gly	Gly	Ala	Tyr
	995						1000					1005			
Gly	Ala	Thr	Ala	Asp	Met	Ser	Ala	Lys	Ile	Gly	Gly	Glu	Gly	Asp	Leu
	1010					1015				1020					
Ala	Ile	Asn	Thr	Val	Arg	Gln	Val	Ser	Leu	Ser	Asn	Gly	Gln	Asn	Asp
	1025				1030					1035					1040
Tyr	Gln	Gly	Ala	Thr	Tyr	Val	Gln	Met	Gly	Thr	Leu	Arg	Thr	Asp	Ala
			1045						1050					1055	
Asp	Gly	Ala	Leu	Gly	Asn	Thr	Arg	Glu	Leu	Asn	Ile	Ser	Asn	Ala	Ala
		1060						1065					1070		
Ile	Val	Asp	Leu	Asn	Gly	Ser	Thr	Gln	Thr	Val	Glu	Thr	Phe	Thr	Gly
	1075						1080					1085			
Gln	Met	Gly	Ser	Thr	Val	Leu	Phe	Lys	Glu	Gly	Ala	Leu	Thr	Val	Asn
	1090					1095					1100				
Lys	Gly	Gly	Ile	Ser	Gln	Gly	Glu	Leu	Thr	Gly	Gly	Gly	Asn	Leu	Asn
	1105				1110					1115					1120
Val	Thr	Gly	Gly	Thr	Leu	Ala	Ile	Glu	Gly	Leu	Asn	Ala	Arg	Tyr	Asn
			1125						1130					1135	
Ala	Leu	Thr	Ser	Ile	Ser	Pro	Asn	Ala	Glu	Val	Ser	Leu	Asp	Asn	Thr
			1140					1145					1150		
Gln	Gly	Leu	Gly	Arg	Gly	Asn	Ile	Ala	Asn	Asp	Gly	Leu	Leu	Thr	Leu
	1155					1160					1165				
Lys	Asn	Val	Thr	Gly	Glu	Leu	Arg	Asn	Ser	Ile	Ser	Gly	Lys	Gly	Ile
	1170					1175					1180				
Val	Ser	Ala	Thr	Ala	Arg	Thr	Asp	Val	Glu	Leu	Asp	Gly	Asp	Asn	Ser
	1185				1190					1195					1200
Arg	Phe	Val	Gly	Gln	Phe	Asn	Ile	Asp	Thr	Gly	Ser	Ala	Leu	Ser	Val

	1205		1210		1215										
Asn	Glu	Gln	Lys	Asn	Leu	Gly	Asp	Ala	Ser	Val	Ile	Asn	Asn	Gly	Leu
	1220		1225		1230										
Leu	Thr	Ile	Ser	Thr	Glu	Arg	Ser	Trp	Ala	Met	Thr	His	Ser	Ile	Ser
	1235		1240		1245										
Gly	Ser	Gly	Asp	Val	Thr	Lys	Leu	Gly	Thr	Gly	Ile	Leu	Thr	Leu	Asn
	1250		1255		1260										
Asn	Asp	Ser	Ala	Ala	Tyr	Gln	Gly	Thr	Thr	Asp	Ile	Val	Gly	Gly	Glu
1265			1270		1275										1280
Ile	Ala	Phe	Gly	Ser	Asp	Ser	Ala	Ile	Asn	Met	Ala	Ser	Gln	His	Ile
	1285		1290		1295										
Asn	Ile	His	Asn	Ser	Gly	Val	Met	Ser	Gly	Asn	Val	Thr	Thr	Ala	Gly
	1300		1305		1310										
Asp	Met	Asn	Val	Met	Pro	Gly	Gly	Gly	Thr	Ala	Cys	Arg			
	1315		1320												

<210> 305
 <211> 251
 <212> PRT
 <213> Escherichia coli

<400> 305

Met	Thr	Glu	Ala	Gln	Arg	His	Gln	Ile	Leu	Leu	Glu	Met	Leu	Ala	Gln
1				5					10					15	
Leu	Gly	Phe	Val	Thr	Val	Glu	Lys	Val	Val	Glu	Arg	Leu	Gly	Ile	Ser
			20					25					30		
Pro	Ala	Thr	Ala	Arg	Arg	Asp	Ile	Asn	Lys	Leu	Asp	Glu	Ser	Gly	Lys
			35				40					45			
Leu	Lys	Lys	Val	Arg	Asn	Gly	Ala	Glu	Ala	Ile	Thr	Gln	Gln	Arg	Pro
	50					55					60				
Arg	Trp	Thr	Pro	Met	Asn	Leu	His	Gln	Ala	Gln	Asn	His	Asp	Glu	Lys
65					70					75				80	
Val	Arg	Ile	Ala	Lys	Ala	Ala	Ser	Gln	Leu	Val	Asn	Pro	Gly	Glu	Ser
				85					90					95	
Val	Val	Ile	Asn	Cys	Gly	Ser	Thr	Ala	Phe	Leu	Leu	Gly	Arg	Glu	Met
			100					105					110		
Cys	Gly	Lys	Pro	Val	Gln	Ile	Ile	Thr	Asn	Tyr	Leu	Pro	Leu	Ala	Asn
	115						120					125			
Tyr	Leu	Ile	Asp	Gln	Glu	His	Asp	Ser	Val	Ile	Ile	Met	Gly	Gly	Gln
	130					135					140				
Tyr	Asn	Lys	Ser	Gln	Ser	Ile	Thr	Leu	Ser	Pro	Gln	Gly	Ser	Glu	Asn
145					150					155					160
Ser	Leu	Tyr	Ala	Gly	His	Trp	Met	Phe	Thr	Ser	Gly	Lys	Gly	Leu	Thr
				165					170					175	
Ala	Glu	Gly	Leu	Tyr	Lys	Thr	Asp	Met	Leu	Thr	Ala	Met	Ala	Glu	Gln
			180					185					190		
Lys	Met	Leu	Ser	Val	Val	Gly	Lys	Leu	Val	Val	Leu	Val	Asp	Ser	Ser
	195						200					205			
Lys	Ile	Gly	Glu	Arg	Ala	Gly	Met	Leu	Phe	Ser	Arg	Ala	Asp	Gln	Ile
	210					215					220				
Asp	Met	Leu	Ile	Thr	Gly	Lys	Asn	Ala	Asn	Pro	Glu	Ile	Leu	Gln	Gln
225					230					235					240
Leu	Glu	Ala	Gln	Gly	Val	Ser	Ile	Leu	Arg	Val					
			245					250							

<210> 306
 <211> 274
 <212> PRT
 <213> Escherichia coli

<400> 306

Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
 1 5 10 15
 Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
 20 25 30
 His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
 35 40 45
 Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
 50 55 60
 Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
 65 70 75 80
 Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
 85 90 95
 Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
 100 105 110
 Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
 115 120 125
 His His Asp His Glu His His His Asp His Gly His His His His
 130 135 140
 Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
 145 150 155 160
 Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
 165 170 175
 Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
 180 185 190
 Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
 195 200 205
 Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
 210 215 220
 Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
 225 230 235 240
 Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
 245 250 255
 Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
 260 265 270
 Met Arg

<210> 307
 <211> 172
 <212> PRT
 <213> Escherichia coli

<400> 307

Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys

50	55	60
Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp		
65	70	75
Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys		80
	85	90
Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly		95
	100	105
Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln		110
	115	120
Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr		125
	130	135
Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile		140
145	150	155
Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg		160
	165	170

<210> 308
 <211> 344
 <212> PRT
 <213> Escherichia coli

<400> 308
Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
1 5 10 15
Val Ser Tyr Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
20 25 30
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
35 40 45
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
50 55 60
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
65 70 75 80
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
85 90 95
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
100 105 110
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
115 120 125
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
130 135 140
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
145 150 155 160
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
165 170 175
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
180 185 190
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
195 200 205
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
210 215 220
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
225 230 235 240
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
245 250 255
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
260 265 270

Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 309
 <211> 826
 <212> PRT
 <213> Escherichia coli

<400> 309
 Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1 5 10 15
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125
 Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
 130 135 140
 Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
 145 150 155 160
 Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
 165 170 175
 Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
 180 185 190
 Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys
 195 200 205
 Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
 210 215 220
 Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
 225 230 235 240
 Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
 245 250 255
 Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
 260 265 270
 Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
 275 280 285
 Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
 290 295 300
 Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr

Val	Asn	Asp	Ile	His	Gly	His	Asn	Ile	Gly	Val	Val	Gly	Gln	Gly	Ser
770						775				780					
Gln	Leu	Phe	Ile	Arg	Thr	Asn	Glu	Val	Pro	Pro	Ser	Val	Asn	Val	Ala
785						790				795					800
Ile	Asp	Lys	Gln	Gln	Gly	Leu	Ser	Cys	Thr	Ile	Thr	Phe	Gly	Lys	Glu
			805						810					815	
Ile	Asp	Glu	Ser	Arg	Asn	Tyr	Ile	Cys	Gln						
		820						825							

<210> 310
 <211> 239
 <212> PRT
 <213> Escherichia coli

Met	Ala	Ala	Ile	Pro	Trp	Arg	Pro	Phe	Asn	Leu	Arg	Gly	Ile	Lys	Met
1				5					10					15	
Lys	Gly	Leu	Leu	Ser	Leu	Leu	Ile	Phe	Ser	Met	Val	Leu	Pro	Ala	His
		20						25					30		
Ala	Gly	Ile	Val	Ile	Tyr	Gly	Thr	Arg	Ile	Ile	Tyr	Pro	Ala	Glu	Asn
		35					40					45			
Lys	Glu	Val	Met	Val	Gln	Leu	Met	Asn	Gln	Gly	Asn	Arg	Ser	Ser	Leu
	50					55					60				
Leu	Gln	Ala	Trp	Ile	Asp	Asp	Gly	Asp	Thr	Ser	Leu	Pro	Pro	Glu	Lys
65					70					75					80
Ile	Gln	Val	Pro	Phe	Met	Leu	Thr	Pro	Pro	Val	Ala	Lys	Ile	Gly	Ala
				85					90					95	
Asn	Ser	Gly	Gln	Gln	Val	Lys	Ile	Lys	Ile	Met	Pro	Asn	Lys	Leu	Pro
			100					105					110		
Thr	Asn	Lys	Glu	Ser	Ile	Phe	Tyr	Leu	Asn	Val	Leu	Asp	Ile	Pro	Pro
		115					120					125			
Asn	Ser	Pro	Glu	Gln	Glu	Gly	Lys	Asn	Ala	Leu	Lys	Phe	Ala	Met	Gln
		130				135					140				
Asn	Arg	Ile	Lys	Leu	Phe	Tyr	Arg	Pro	Ala	Gly	Ile	Ala	Pro	Val	Asn
145					150					155					160
Lys	Ala	Thr	Phe	Lys	Lys	Leu	Leu	Val	Asn	Arg	Ser	Gly	Asn	Gly	Leu
			165						170					175	
Val	Ile	Lys	Asn	Asp	Ser	Ala	Asn	Trp	Val	Thr	Ile	Ser	Asp	Val	Lys
			180					185					190		
Ala	Asn	Asn	Val	Lys	Val	Asn	Tyr	Glu	Thr	Ile	Met	Ile	Ala	Pro	Leu
	195						200					205			
Glu	Ser	Gln	Ser	Val	Asn	Val	Lys	Ser	Asn	Asn	Ala	Asn	Asn	Trp	His
	210					215					220				
Leu	Thr	Ile	Ile	Asp	Asp	His	Gly	Asn	Tyr	Ile	Ser	Asp	Lys	Ile	
225					230					235					

<210> 311
 <211> 180
 <212> PRT
 <213> Escherichia coli

Met	Lys	Arg	Ser	Ile	Ile	Ala	Ala	Ala	Val	Phe	Ser	Ser	Phe	Phe	Met
1				5					10					15	
Ser	Ala	Gly	Val	Phe	Ala	Ala	Asp	Val	Asp	Thr	Gly	Thr	Leu	Thr	Ile

Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala
65 70 75 80
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val
85 90 95
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn
100 105 110
Tyr Asp Val Ile Leu Arg Phe
115

<210> 314
<211> 128
<212> PRT
<213> Escherichia coli

<400> 314
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln
1 5 10 15
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His
20 25 30
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn
35 40 45
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp
50 55 60
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala
65 70 75 80
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu
85 90 95
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu
100 105 110
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe
115 120 125

<210> 315
<211> 244
<212> PRT
<213> Escherichia coli

<400> 315
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu
1 5 10 15
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile
20 25 30
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly
35 40 45
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser
50 55 60
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser
65 70 75 80
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala
85 90 95
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val
100 105 110
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val
115 120 125
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln

130		135		140
Ile Met Ser Thr Phe Val	Pro Pro Glu Thr	Pro Asp Val Gly Ser Ser		
145	150	155		160
Val Asn Phe Ala Ser Ser	Val Glu Asp Leu Val	Thr Gln Thr Leu Glu		
	165	170		175
Phe Thr Ile Glu Val	Asn Ala Asp Arg	Asn Val Ser Asn Asn Ala		
	180	185		190
Lys Asn Arg Gln Ile Val	Leu Asn Leu Tyr Glu Lys	Gly Ile Phe Asp		
	195	200		205
Ile Lys Asp Ala Ile Asn	Gln Val Ala Asp Arg	Leu Asn Ile Ser Lys		
	210	215		220
His Thr Val Tyr Leu Tyr	Ile Arg Gln Phe Lys	Ser Gly Asp Phe Gln		
225	230	235		240
Gly Gln Asp Lys				

<210> 316
 <211> 84
 <212> PRT
 <213> Escherichia coli

<400> 316
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
1 5 10 15
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
20 25 30
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
35 40 45
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
50 55 60
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
65 70 75 80
Lys Ala Val Leu

<210> 317
 <211> 63
 <212> PRT
 <213> Escherichia coli

<400> 317
Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
1 5 10 15
Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
20 25 30
Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
35 40 45
Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
50 55 60

<210> 318
 <211> 136
 <212> PRT
 <213> Escherichia coli

<400> 318
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125
 Thr Phe Val Thr Lys Thr Val Met
 130 135

<210> 319
 <211> 233
 <212> PRT
 <213> Escherichia coli

<400> 319
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220
 Lys Lys Gln Gln Arg Lys Gly Arg Lys

225

230

<210> 320

<211> 110

<212> PRT

<213> Escherichia coli

<400> 320

Met	Glu	Thr	Ile	Ala	Lys	His	Arg	His	Ala	Arg	Ser	Ser	Ala	Gln	Lys
1				5					10					15	
Val	Arg	Leu	Val	Ala	Asp	Leu	Ile	Arg	Gly	Lys	Lys	Val	Ser	Gln	Ala
			20					25					30		
Leu	Asp	Ile	Leu	Thr	Tyr	Thr	Asn	Lys	Lys	Ala	Ala	Val	Leu	Val	Lys
		35					40					45			
Lys	Val	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Ala	Glu	His	Asn	Asp	Gly	Ala
		50				55					60				
Asp	Ile	Asp	Asp	Leu	Lys	Val	Thr	Lys	Ile	Phe	Val	Asp	Glu	Gly	Pro
65					70					75					80
Ser	Met	Lys	Arg	Ile	Met	Pro	Arg	Ala	Lys	Gly	Arg	Ala	Asp	Arg	Ile
				85					90					95	
Leu	Lys	Arg	Thr	Ser	His	Ile	Thr	Val	Val	Val	Ser	Asp	Arg		
			100					105					110		

<210> 321

<211> 92

<212> PRT

<213> Escherichia coli

<400> 321

Met	Pro	Arg	Ser	Leu	Lys	Lys	Gly	Pro	Phe	Ile	Asp	Leu	His	Leu	Leu
1				5					10					15	
Lys	Lys	Val	Glu	Lys	Ala	Val	Glu	Ser	Gly	Asp	Lys	Lys	Pro	Leu	Arg
			20					25					30		
Thr	Trp	Ser	Arg	Arg	Ser	Thr	Ile	Phe	Pro	Asn	Met	Ile	Gly	Leu	Thr
		35				40						45			
Ile	Ala	Val	His	Asn	Gly	Arg	Gln	His	Val	Pro	Val	Phe	Val	Thr	Asp
	50				55						60				
Glu	Met	Val	Gly	His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr
65					70				75						80
Arg	Gly	His	Ala	Ala	Asp	Lys	Lys	Ala	Lys	Lys	Lys				
			85					90							

<210> 322

<211> 273

<212> PRT

<213> Escherichia coli

<400> 322

Met	Ala	Val	Val	Lys	Cys	Lys	Pro	Thr	Ser	Pro	Gly	Arg	Arg	His	Val
1				5					10					15	
Val	Lys	Val	Val	Asn	Pro	Glu	Leu	His	Lys	Gly	Lys	Pro	Phe	Ala	Pro
			20					25					30		
Leu	Leu	Glu	Lys	Asn	Ser	Lys	Ser	Gly	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35					40					45			

<213> Escherichia coli

<400> 324

Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1 5 10 15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
20 25 30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
35 40 45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50 55 60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65 70 75 80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
85 90 95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
100 105 110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
115 120 125
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
130 135 140
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
145 150 155 160
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
165 170 175
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
180 185 190
Val Lys Gln Val Glu Glu Met Leu Ala
195 200

<210> 325

<211> 209

<212> PRT

<213> Escherichia coli

<400> 325

Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
1 5 10 15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
20 25 30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
35 40 45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
50 55 60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65 70 75 80
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
85 90 95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
100 105 110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
115 120 125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
130 135 140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
145 150 155 160

Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
165 170 175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
180 185 190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
195 200 205
Ala

<210> 326
<211> 103
<212> PRT
<213> Escherichia coli

<400> 326
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
1 5 10 15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
20 25 30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
35 40 45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
50 55 60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65 70 75 80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
85 90 95
Asp Val Gln Ile Ser Leu Gly
100

<210> 327
<211> 104
<212> PRT
<213> Escherichia coli

<400> 327
Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
1 5 10 15
Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
20 25 30
Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
35 40 45
Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
50 55 60
Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
65 70 75 80
Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
85 90 95
Leu Gln Glu Val Phe Tyr Leu Pro
100

<210> 328
<211> 287
<212> PRT

<213> Escherichia coli

<400> 328

Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
1 5 10 15
Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
20 25 30
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val
35 40 45
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys
50 55 60
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu
65 70 75 80
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys
85 90 95
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp
100 105 110
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala
115 120 125
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala
130 135 140
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu
145 150 155 160
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu
165 170 175
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala
180 185 190
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu
195 200 205
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His
210 215 220
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg
225 230 235 240
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu
245 250 255
Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
260 265 270
Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu
275 280 285

<210> 329

<211> 163

<212> PRT

<213> Escherichia coli

<400> 329

Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
1 5 10 15
Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
20 25 30
His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
35 40 45
Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
50 55 60
Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
65 70 75 80

Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
85 90 95
Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
100 105 110
Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
115 120 125
Met Gln Cys Phe Tyr His Ile Asn Asn Cys Glu Asp Asp Ser Val
130 135 140
Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu
145 150 155 160
Asp Asn Gly

<210> 330
<211> 648
<212> PRT
<213> Escherichia coli

<400> 330
Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
1 5 10 15
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
20 25 30
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
35 40 45
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
50 55 60
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
65 70 75 80
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
85 90 95
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
100 105 110
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
115 120 125
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
130 135 140
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
145 150 155 160
Ala Gly Gly Glu Trp Ile Val Ser Ala Gly Ala Leu Gly Ser Gly Ile
165 170 175
Phe Gly Phe Ile Asn Arg Leu Leu Ile Pro Thr Gly Leu His Gln Val
180 185 190
Leu Asn Thr Ile Ala Trp Phe Gln Ile Gly Glu Phe Thr Asn Ala Ala
195 200 205
Gly Thr Val Phe His Gly Asp Ile Asn Arg Phe Tyr Ala Gly Asp Gly
210 215 220
Thr Ala Gly Met Phe Met Ser Gly Phe Phe Pro Ile Met Met Phe Gly
225 230 235 240
Leu Pro Gly Ala Ala Leu Ala Met Tyr Phe Ala Ala Pro Lys Glu Arg
245 250 255
Arg Pro Met Val Gly Gly Met Leu Leu Ser Val Ala Val Thr Ala Phe
260 265 270
Leu Thr Gly Val Thr Glu Pro Leu Glu Phe Leu Phe Met Phe Leu Ala
275 280 285
Pro Leu Leu Tyr Leu Leu His Ala Leu Leu Thr Gly Ile Ser Leu Phe

Gly	Val	Asp	Asn	Tyr	Arg	Gly	Pro	Ser	Thr	Ala	Ala	Gln	Met	Thr	Phe
	35						40					45			
Asn	Tyr	Thr	Ser	Thr	Ala	Ser	Asn	Leu	Val	Phe	Tyr	Lys	Pro	Thr	Gln
	50					55				60					
Leu	Gly	Pro	Thr	Gly	Val	Lys	Met	Tyr	Trp	Ser	Tyr	Leu	Asp	Thr	Gly
65					70					75					80
Thr	Gly	Gly	Gly	Ile	Leu	Tyr	Cys	Asn	Thr	Ser	Gly	Arg	Ala	Asn	Pro
				85					90					95	
Gly	Pro	Ile	Thr	Ile	Glu	Asn	Ala	Met	Val	Tyr	Ser	Gly	Lys	Asp	Tyr
			100					105					110		
Gly	Gly	His	Lys	Leu	Phe	Asn	Thr	Ser	Val	Pro	Gly	Leu	Tyr	Tyr	Thr
		115					120					125			
Met	Leu	Ile	Ser	Arg	Val	Trp	Ser	Ala	Tyr	Asp	Thr	Ile	Thr	Asp	Ile
	130					135					140				
Gln	Ser	Pro	Gly	Ile	Tyr	Ile	Gly	Asp	Pro	Ser	Asn	Gln	Glu	Phe	Phe
145					150					155					160
Phe	Ser	Val	Thr	Asp	Ser	Asp	Leu	Gln	Thr	Lys	Gly	Cys	Asn	Lys	Ala
				165					170					175	
Asp	Asp	Tyr	Asp	Lys	Phe	Trp	Ala	Ile	Gly	Gly	Ile	Val	His	Asn	Ile
		180					185						190		
Thr	Val	Glu	Phe	Tyr	Thr	Asp	Thr	Asn	Phe	Asp	Pro	Thr	Leu	Asn	Gln
		195					200					205			
Gln	Val	Gln	Leu	Ser	Ser	Ser	Ser	Asn	Tyr	Leu	Tyr	Ser	Phe	Lys	Ala
	210					215					220				
Tyr	Ser	Pro	Gly	Thr	Lys	Val	Val	Asp	His	Ser	Asn	His	Ile	Tyr	Val
225					230					235					240
Asn	Phe	Thr	Leu	Asn	Val	Lys	Leu	Thr	Leu	Pro	Thr	Cys	Phe	Thr	
				245				250					255		
Ser	Ile	Leu	Thr	Gly	Pro	Ser	Val	Asn	Gly	Ser	Thr	Val	Arg	Met	Gly
		260						265					270		
Glu	Tyr	Ser	Ser	Gly	Thr	Ile	Lys	Asn	Gly	Ala	Ser	Pro	Val	Pro	Phe
		275					280					285			
Asp	Ile	Ser	Leu	Gln	Asn	Cys	Ile	Arg	Val	Arg	Asn	Ile	Glu	Thr	Lys
	290					295					300				
Leu	Val	Thr	Gly	Lys	Val	Gly	Thr	Gln	Asn	Thr	Gln	Leu	Leu	Gly	Asn
305					310					315					320
Thr	Leu	Thr	Gly	Ser	Thr	Ala	Ala	Lys	Gly	Val	Gly	Val	Leu	Ile	Glu
				325					330					335	
Gly	Leu	Ala	Thr	Ser	Lys	Asn	Pro	Leu	Met	Thr	Leu	Lys	Pro	Asn	Asp
		340						345					350		
Thr	Asn	Ser	Val	Tyr	Ile	Asp	Tyr	Glu	Thr	Glu	Asp	Asp	Thr	Ser	Asp
		355					360					365			
Gly	Val	Tyr	Pro	Asn	Gln	Gly	Asn	Gly	Thr	Ser	Gln	Pro	Leu	His	Phe
	370					375					380				
Gln	Ala	Thr	Leu	Lys	Gln	Asp	Gly	Asn	Ile	Ala	Ile	Glu	Pro	Gly	Glu
385					390					395					400
Phe	Lys	Ala	Thr	Ser	Thr	Phe	Gln	Val	Thr	Tyr	Pro				
				405					410						

<210> 332

<211> 198

<212> PRT

<213> Escherichia coli

<400> 332

Met His Pro Thr Gln Arg Lys Leu Met Lys Arg Ile Ile Leu Phe Leu

1	5	10	15
Ser Leu Leu Phe Cys Ile Ala Cys Pro Ala Ile Ala Gly Gln Asp Ile			
20	25	30	
Asp Leu Val Ala Asn Val Lys Asn Ser Thr Cys Lys Ser Gly Ile Ser			
35	40	45	
Asn Gln Gly Asn Ile Asp Leu Gly Val Val Gly Val Gly Tyr Phe Ser			
50	55	60	
Gly Asn Val Thr Pro Glu Ser Tyr Gln Pro Gly Gly Lys Glu Phe Thr			
65	70	75	80
Ile Thr Val Ser Asp Cys Ala Leu Gln Gly Thr Gly Asp Val Leu Asn			
85	90	95	
Gln Leu His Ile Asp Phe Arg Ala Leu Ser Gly Val Met Ala Ala Gly			
100	105	110	
Ser Arg Gln Ile Phe Ala Asn Glu Ile Ser Ser Gly Ala Ser Asn Val			
115	120	125	
Gly Val Val Ile Phe Ser Thr Gln Asp Ser Ala Asn Thr Phe Asn Val			
130	135	140	
Leu Asn Ala Ser Gly Gly Ser Arg Ser Val Tyr Pro Val Met Ser Asp			
145	150	155	160
Asp Met Asn Gly Ser Ser Trp Lys Phe Ser Thr Arg Met Gln Lys Ile			
165	170	175	
Asp Pro Ala Leu Ser Val Thr Ser Gly Gln Leu Met Ser His Val Leu			
180	185	190	
Val Asp Ile Tyr Tyr Glu			
195			

<210> 333
 <211> 201
 <212> PRT
 <213> Escherichia coli

<400> 333
Met Met Thr Phe Lys Asn Leu Arg Tyr Gly Leu Ser Ser Ser Val Val
1 5 10 15
Leu Ala Ala Ser Leu Phe Ser Val Leu Ser Tyr Ala Ala Thr Asp Ser
20 25 30
Ile Gly Leu Thr Val Ile Thr Thr Val Glu Met Gly Thr Cys Thr Ala
35 40 45
Thr Leu Val Asn Asp Ser Asp Gln Asp Ile Ser Val Val Asp Phe Gly
50 55 60
Asp Val Tyr Ile Ser Glu Ile Asn Ala Lys Thr Lys Val Lys Thr Phe
65 70 75 80
Lys Leu Lys Phe Lys Asp Cys Ala Gly Ile Pro Asn Lys Lys Ala Gln
85 90 95
Ile Lys Leu Thr Lys Arg Ala Thr Cys Glu Gly Thr Ala Asn Asp Gly
100 105 110
Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val
115 120 125
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr
130 135 140
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr
145 150 155 160
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val
165 170 175
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala
180 185 190

Pro Ala Thr Phe Thr Val Thr Tyr Asn
195 200

<210> 334
<211> 203
<212> PRT
<213> Escherichia coli

<400> 334
Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile
1 5 10 15
Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser
20 25 30
Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val
35 40 45
Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn
50 55 60
Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp
65 70 75 80
Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val
85 90 95
Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
100 105 110
Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
115 120 125
Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
130 135 140
Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
145 150 155 160
Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
165 170 175
Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
180 185 190
Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln
195 200

<210> 335
<211> 139
<212> PRT
<213> Escherichia coli

<400> 335
Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
1 5 10 15
Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
20 25 30
Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
35 40 45
Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
50 55 60
Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
65 70 75 80
Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
85 90 95
Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp

	100		105		110										
Val	Asp	Tyr	Ala	Gln	Ala	Ser	Ala	Glu	Leu	Ala	Lys	Ala	Ile	Ala	Gln
	115		120		125										
Leu	Arg	Val	Ile	Glu	Leu	Thr	Lys	Lys	Ala	Met					
	130					135									

<210> 336
 <211> 460
 <212> PRT
 <213> Escherichia coli

<400> 336

Met	Ala	Thr	Gly	Lys	Ile	Val	Gln	Val	Ile	Gly	Ala	Val	Val	Asp	Val
1				5					10					15	
Glu	Phe	Pro	Gln	Asp	Ala	Val	Pro	Arg	Val	Tyr	Asp	Ala	Leu	Glu	Val
			20					25					30		
Gln	Asn	Gly	Asn	Glu	Arg	Leu	Val	Leu	Glu	Val	Gln	Gln	Gln	Leu	Gly
		35					40					45			
Gly	Gly	Ile	Val	Arg	Thr	Ile	Ala	Met	Gly	Ser	Ser	Asp	Gly	Leu	Arg
	50				55						60				
Arg	Gly	Leu	Asp	Val	Lys	Asp	Leu	Glu	His	Pro	Ile	Glu	Val	Pro	Val
	65				70					75				80	
Gly	Lys	Ala	Thr	Leu	Gly	Arg	Ile	Met	Asn	Val	Leu	Gly	Glu	Pro	Val
				85					90					95	
Asp	Met	Lys	Gly	Glu	Ile	Gly	Glu	Glu	Arg	Trp	Ala	Ile	His	Arg	
			100					105					110		
Ala	Ala	Pro	Ser	Tyr	Glu	Glu	Leu	Ser	Asn	Ser	Gln	Glu	Leu	Leu	Glu
		115					120					125			
Thr	Gly	Ile	Lys	Val	Ile	Asp	Leu	Met	Cys	Pro	Phe	Ala	Lys	Gly	Gly
	130					135					140				
Lys	Val	Gly	Leu	Phe	Gly	Gly	Ala	Gly	Val	Gly	Lys	Thr	Val	Asn	Met
	145				150					155				160	
Met	Glu	Leu	Ile	Arg	Asn	Ile	Ala	Ile	Glu	His	Ser	Gly	Tyr	Ser	Val
				165					170					175	
Phe	Ala	Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Phe	Tyr	His
			180				185					190			
Glu	Met	Thr	Asp	Ser	Asn	Val	Ile	Asp	Lys	Val	Ser	Leu	Val	Tyr	Gly
		195				200						205			
Gln	Met	Asn	Glu	Pro	Pro	Gly	Asn	Arg	Leu	Arg	Val	Ala	Leu	Thr	Gly
	210					215					220				
Leu	Thr	Met	Ala	Glu	Lys	Phe	Arg	Asp	Glu	Gly	Arg	Asp	Val	Leu	Leu
	225				230					235				240	
Phe	Val	Asp	Asn	Ile	Tyr	Arg	Tyr	Thr	Leu	Ala	Gly	Thr	Glu	Val	Ser
			245						250					255	
Ala	Leu	Leu	Gly	Arg	Met	Pro	Ser	Ala	Val	Gly	Tyr	Gln	Pro	Thr	Leu
			260					265					270		
Ala	Glu	Glu	Met	Gly	Val	Leu	Gln	Glu	Arg	Ile	Thr	Ser	Thr	Lys	Thr
		275					280					285			
Gly	Ser	Ile	Thr	Ser	Val	Gln	Ala	Val	Tyr	Val	Pro	Ala	Asp	Asp	Leu
	290					295					300				
Thr	Asp	Pro	Ser	Pro	Ala	Thr	Thr	Phe	Ala	His	Leu	Asp	Ala	Thr	Val
	305				310					315				320	
Val	Leu	Ser	Arg	Gln	Ile	Ala	Ser	Leu	Gly	Ile	Tyr	Pro	Ala	Val	Asp
			325						330					335	
Pro	Leu	Asp	Ser	Thr	Ser	Arg	Gln	Leu	Asp	Pro	Leu	Val	Val	Gly	Gln
			340					345					350		

Glu His Tyr Asp Thr Ala Arg Gly Val Gln Ser Ile Leu Gln Arg Tyr
 355 360 365
 Gln Glu Leu Lys Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser
 370 375 380
 Glu Glu Asp Lys Leu Val Val Ala Arg Ala Arg Lys Ile Gln Arg Phe
 385 390 395 400
 Leu Ser Gln Pro Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly
 405 410 415
 Lys Tyr Val Ser Leu Lys Asp Thr Ile Arg Gly Phe Lys Gly Ile Met
 420 425 430
 Glu Gly Glu Tyr Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly
 435 440 445
 Ser Ile Glu Glu Ala Val Glu Lys Ala Lys Lys Leu
 450 455 460

<210> 337
 <211> 287
 <212> PRT
 <213> Escherichia coli

<400> 337
 Met Ala Gly Ala Lys Glu Ile Arg Ser Lys Ile Ala Ser Val Gln Asn
 1 5 10 15
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
 20 25 30
 Arg Lys Ser Gln Asp Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Thr
 35 40 45
 Met Arg Lys Val Ile Gly His Leu Ala His Gly Asn Leu Glu Tyr Lys
 50 55 60
 His Pro Tyr Leu Glu Asp Arg Asp Val Lys Arg Val Gly Tyr Leu Val
 65 70 75 80
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95
 Lys Lys Leu Leu Ala Glu Met Lys Thr Trp Thr Asp Lys Gly Val Gln
 100 105 110
 Cys Asp Leu Ala Met Ile Gly Ser Lys Gly Val Ser Phe Phe Asn Ser
 115 120 125
 Val Gly Gly Asn Val Val Ala Gln Val Thr Gly Met Gly Asp Asn Pro
 130 135 140
 Ser Leu Ser Glu Leu Ile Gly Pro Val Lys Val Met Leu Gln Ala Tyr
 145 150 155 160
 Asp Glu Gly Arg Leu Asp Lys Leu Tyr Ile Val Ser Asn Lys Phe Ile
 165 170 175
 Asn Thr Met Ser Gln Val Pro Thr Ile Ser Gln Leu Leu Pro Leu Pro
 180 185 190
 Ala Ser Asp Asp Asp Asp Leu Lys His Lys Ser Trp Asp Tyr Leu Tyr
 195 200 205
 Glu Pro Asp Pro Lys Ala Leu Leu Asp Thr Leu Leu Arg Arg Tyr Val
 210 215 220
 Glu Ser Gln Val Tyr Gln Gly Val Val Glu Asn Leu Ala Ser Glu Gln
 225 230 235 240
 Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Gly Gly Ser
 245 250 255
 Leu Ile Lys Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala Ser
 260 265 270
 Ile Thr Gln Glu Leu Thr Glu Ile Val Ser Gly Ala Ala Ala Val

<210> 338
 <211> 513
 <212> PRT
 <213> Escherichia coli

<400> 338

Met	Gln	Leu	Asn	Ser	Thr	Glu	Ile	Ser	Glu	Leu	Ile	Lys	Gln	Arg	Ile
1				5					10					15	
Ala	Gln	Phe	Asn	Val	Val	Ser	Glu	Ala	His	Asn	Glu	Gly	Thr	Ile	Val
			20					25					30		
Ser	Val	Ser	Asp	Gly	Val	Ile	Arg	Ile	His	Gly	Leu	Ala	Asp	Cys	Met
		35					40					45			
Gln	Gly	Glu	Met	Ile	Ser	Leu	Pro	Gly	Asn	Arg	Tyr	Ala	Ile	Ala	Leu
	50					55					60				
Asn	Leu	Glu	Arg	Asp	Ser	Val	Gly	Ala	Val	Val	Met	Gly	Pro	Tyr	Ala
65					70					75					80
Asp	Leu	Ala	Glu	Gly	Met	Lys	Val	Lys	Cys	Thr	Gly	Arg	Ile	Leu	Glu
				85					90					95	
Val	Pro	Val	Gly	Arg	Gly	Leu	Leu	Gly	Arg	Val	Val	Asn	Thr	Leu	Gly
			100					105					110		
Ala	Pro	Ile	Asp	Gly	Lys	Gly	Pro	Leu	Asp	His	Asp	Gly	Phe	Ser	Ala
		115					120					125			
Val	Glu	Ala	Ile	Ala	Pro	Gly	Val	Ile	Glu	Arg	Gln	Ser	Val	Asp	Gln
	130					135					140				
Pro	Val	Gln	Thr	Gly	Tyr	Lys	Ala	Val	Asp	Ser	Met	Ile	Pro	Ile	Gly
145					150					155					160
Arg	Gly	Gln	Arg	Glu	Leu	Ile	Ile	Gly	Asp	Arg	Gln	Thr	Gly	Lys	Thr
				165					170					175	
Ala	Leu	Ala	Ile	Asp	Ala	Ile	Ile	Asn	Gln	Arg	Asp	Ser	Gly	Ile	Lys
			180					185					190		
Cys	Ile	Tyr	Val	Ala	Ile	Gly	Gln	Lys	Ala	Ser	Thr	Ile	Ser	Asn	Val
	195						200					205			
Val	Arg	Lys	Leu	Glu	Glu	His	Gly	Ala	Leu	Ala	Asn	Thr	Ile	Val	Val
	210					215					220				
Val	Ala	Thr	Ala	Ser	Glu	Ser	Ala	Ala	Leu	Gln	Tyr	Leu	Ala	Pro	Tyr
225					230					235				240	
Ala	Gly	Cys	Ala	Met	Gly	Glu	Tyr	Phe	Arg	Asp	Arg	Gly	Glu	Asp	Ala
				245					250					255	
Leu	Ile	Ile	Tyr	Asp	Asp	Leu	Ser	Lys	Gln	Ala	Val	Ala	Tyr	Arg	Gln
			260					265					270		
Ile	Ser	Leu	Leu	Leu	Arg	Arg	Pro	Pro	Gly	Arg	Glu	Ala	Phe	Pro	Gly
	275						280					285			
Asp	Val	Phe	Tyr	Leu	His	Ser	Arg	Leu	Leu	Glu	Arg	Ala	Ala	Arg	Val
	290					295					300				
Asn	Ala	Glu	Tyr	Val	Glu	Ala	Phe	Thr	Lys	Gly	Glu	Val	Lys	Gly	Lys
305					310					315				320	
Thr	Gly	Ser	Leu	Thr	Ala	Leu	Pro	Ile	Ile	Glu	Thr	Gln	Ala	Gly	Asp
				325					330					335	
Val	Ser	Ala	Phe	Val	Pro	Thr	Asn	Val	Ile	Ser	Ile	Thr	Asp	Gly	Gln
			340				345						350		
Ile	Phe	Leu	Glu	Thr	Asn	Leu	Phe	Asn	Ala	Gly	Ile	Arg	Pro	Ala	Val
	355					360						365			
Asn	Pro	Gly	Ile	Ser	Val	Ser	Arg	Val	Gly	Gly	Ala	Ala	Gln	Thr	Lys
	370					375					380				

Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr
 385 390 395 400
 Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala
 405 410 415
 Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys
 420 425 430
 Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu
 435 440 445
 Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile
 450 455 460
 Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala
 465 470 475 480
 Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile
 485 490 495
 Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser
 500 505 510
 Trp

<210> 339
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 339
 Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu
 20 25 30
 Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu
 35 40 45
 Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val
 50 55 60
 Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met
 65 70 75 80
 Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe
 85 90 95
 Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile
 100 105 110
 Ser Ala Ala Ala Leu Ser Glu Gln Leu Ala Lys Ile Ser Ala Ala
 115 120 125
 Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp
 130 135 140
 Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile
 145 150 155 160
 Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln
 165 170 175
 Ser

<210> 340
 <211> 156
 <212> PRT
 <213> Escherichia coli

<400> 340

Met	Asn	Leu	Asn	Ala	Thr	Ile	Leu	Gly	Gln	Ala	Ile	Ala	Phe	Val	Leu
1			5					10						15	
Phe	Val	Leu	Phe	Cys	Met	Lys	Tyr	Val	Trp	Pro	Pro	Leu	Met	Ala	Ala
		20						25				30			
Ile	Glu	Lys	Arg	Gln	Lys	Glu	Ile	Ala	Asp	Gly	Leu	Ala	Ser	Ala	Glu
		35				40						45			
Arg	Ala	His	Lys	Asp	Leu	Asp	Leu	Ala	Lys	Ala	Ser	Ala	Thr	Asp	Gln
	50					55					60				
Leu	Lys	Lys	Ala	Lys	Ala	Glu	Ala	Gln	Val	Ile	Ile	Glu	Gln	Ala	Asn
65				70						75					80
Lys	Arg	Arg	Ser	Gln	Ile	Leu	Asp	Glu	Ala	Lys	Ala	Glu	Ala	Glu	Gln
			85					90						95	
Glu	Arg	Thr	Lys	Ile	Val	Ala	Gln	Ala	Gln	Ala	Glu	Ile	Glu	Ala	Glu
			100					105					110		
Arg	Lys	Arg	Ala	Arg	Glu	Glu	Leu	Arg	Lys	Gln	Val	Ala	Ile	Leu	Ala
		115					120					125			
Val	Ala	Gly	Ala	Glu	Lys	Ile	Ile	Glu	Arg	Ser	Val	Asp	Glu	Ala	Ala
	130					135					140				
Asn	Ser	Asp	Ile	Val	Asp	Lys	Leu	Val	Ala	Glu	Leu				
145					150						155				

<210> 341

<211> 79

<212> PRT

<213> Escherichia coli

<400> 341

Met	Glu	Asn	Leu	Asn	Met	Asp	Leu	Leu	Tyr	Met	Ala	Ala	Ala	Val	Met
1				5					10					15	
Met	Gly	Leu	Ala	Ala	Ile	Gly	Ala	Ala	Ile	Gly	Ile	Gly	Ile	Leu	Gly
		20						25					30		
Gly	Lys	Phe	Leu	Glu	Gly	Ala	Ala	Arg	Gln	Pro	Asp	Leu	Ile	Pro	Leu
		35				40						45			
Leu	Arg	Thr	Gln	Phe	Phe	Ile	Val	Met	Gly	Leu	Val	Asp	Ala	Ile	Pro
	50				55						60				
Met	Ile	Ala	Val	Gly	Leu	Gly	Leu	Tyr	Val	Met	Phe	Ala	Val	Ala	
65					70					75					

<210> 342

<211> 271

<212> PRT

<213> Escherichia coli

<400> 342

Met	Ala	Ser	Glu	Asn	Met	Thr	Pro	Gln	Asp	Tyr	Ile	Gly	His	His	Leu
1				5					10					15	
Asn	Asn	Leu	Gln	Leu	Asp	Leu	Arg	Thr	Phe	Ser	Leu	Val	Asp	Pro	Gln
		20						25					30		
Asn	Pro	Pro	Ala	Thr	Phe	Trp	Thr	Ile	Asn	Ile	Asp	Ser	Met	Phe	Phe
		35				40						45			
Ser	Val	Val	Leu	Gly	Leu	Leu	Phe	Leu	Val	Leu	Phe	Arg	Ser	Val	Ala
	50				55						60				
Lys	Lys	Ala	Thr	Ser	Gly	Val	Pro	Gly	Lys	Phe	Gln	Thr	Ala	Ile	Glu
65					70					75					80

Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
 85 90 95
 Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
 100 105 110
 Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
 115 120 125
 Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
 130 135 140
 Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
 145 150 155 160
 Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
 165 170 175
 Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn
 180 185 190
 Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly
 195 200 205
 Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu
 210 215 220
 Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro
 225 230 235 240
 Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe
 245 250 255
 Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His
 260 265 270

<210> 343
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 343
 Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg
 1 5 10 15
 Lys Leu Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu
 20 25 30
 Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly
 35 40 45
 Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg
 50 55 60
 His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala
 65 70 75 80
 Phe Gly Glu Ala Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val
 85 90 95
 Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp
 100 105 110
 Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn
 115 120 125
 Lys Gly
 130

<210> 344
 <211> 413
 <212> PRT
 <213> Escherichia coli

<212> PRT
 <213> Escherichia coli

<400> 345

Met	Ser	Ser	Ile	Ser	Leu	Ile	Gln	Pro	Asp	Arg	Asp	Leu	Phe	Ser	Trp
1				5					10					15	
Pro	Gln	Tyr	Trp	Ala	Ala	Cys	Phe	Gly	Pro	Ala	Pro	Phe	Leu	Pro	Met
			20					25					30		
Ser	Arg	Glu	Glu	Met	Asp	Gln	Leu	Gly	Trp	Asp	Ser	Cys	Asp	Ile	Ile
		35					40					45			
Leu	Val	Thr	Gly	Asp	Ala	Tyr	Val	Asp	His	Pro	Ser	Phe	Gly	Met	Ala
	50					55					60				
Ile	Cys	Gly	Arg	Met	Leu	Glu	Ala	Gln	Gly	Phe	Arg	Val	Gly	Ile	Ile
65					70					75					80
Ala	Gln	Pro	Asp	Trp	Ser	Ser	Lys	Asp	Asp	Phe	Met	Arg	Leu	Gly	Lys
			85						90					95	
Pro	Asn	Leu	Phe	Phe	Gly	Val	Thr	Ala	Gly	Asn	Met	Asp	Ser	Met	Ile
			100					105					110		
Asn	Arg	Tyr	Thr	Ala	Asp	Arg	Arg	Leu	Arg	His	Asp	Asp	Ala	Tyr	Thr
		115				120						125			
Pro	Asp	Asn	Val	Ala	Gly	Lys	Arg	Pro	Asp	Arg	Ala	Thr	Leu	Val	Tyr
	130					135					140				
Thr	Gln	Arg	Cys	Lys	Glu	Ala	Trp	Lys	Asp	Val	Pro	Val	Ile	Leu	Gly
145					150					155					160
Gly	Ile	Glu	Ala	Ser	Leu	Arg	Arg	Thr	Ala	His	Tyr	Asp	Tyr	Trp	Ser
				165					170					175	
Asp	Thr	Val	Arg	Arg	Ser	Val	Leu	Val	Asp	Ser	Lys	Ala	Asp	Met	Leu
			180					185					190		
Met	Phe	Gly	Asn	Gly	Glu	Arg	Pro	Leu	Val	Glu	Val	Ala	His	Arg	Leu
		195					200					205			
Ala	Met	Gly	Glu	Pro	Ile	Ser	Glu	Ile	Arg	Asp	Val	Arg	Asn	Thr	Ala
	210					215					220				
Ile	Ile	Val	Lys	Glu	Ala	Leu	Pro	Gly	Trp	Ser	Gly	Val	Asp	Ser	Thr
225					230					235					240
Arg	Leu	Asp	Thr	Pro	Gly	Lys	Ile	Asp	Pro	Ile	Pro	His	Pro	Tyr	Gly
			245					250						255	
Glu	Asp	Leu	Pro	Cys	Ala	Asp	Asn	Lys	Pro	Val	Ala	Pro	Lys	Lys	Gln
		260					265						270		
Glu	Ala	Lys	Ala	Val	Thr	Val	Gln	Pro	Pro	Arg	Pro	Lys	Pro	Trp	Glu
	275						280					285			
Lys	Thr	Tyr	Val	Leu	Leu	Pro	Ser	Phe	Glu	Lys	Val	Lys	Gly	Asp	Lys
	290					295					300				
Val	Leu	Tyr	Ala	His	Ala	Ser	Arg	Ile	Leu	His	His	Glu	Thr	Asn	Pro
305					310					315					320
Ala	Val	Pro	Ala	His											
				325											

<210> 346
 <211> 226
 <212> PRT
 <213> Escherichia coli

<400> 346

Met	Ile	Gln	Tyr	Leu	Asn	Val	Phe	Phe	Tyr	Asp	Ile	Tyr	Pro	Tyr	Ile
1				5					10					15	
Cys	Ala	Thr	Val	Phe	Phe	Leu	Gly	Ser	Trp	Leu	Arg	Tyr	Asp	Tyr	Gly

Asp	Asp	Thr	Arg	Gln	Ala	Leu	Asp	Ala	Val	Trp	Glu	Glu	Glu	Gln	Val
			180					185					190		
Lys	Phe	Ile	Glu	Asp	Asn	Ala	Thr	Ala	Cys	Asp	Ser	Ser	Pro	Leu	Asn
		195					200					205			
Gln	Tyr	Gln	Arg	Arg	Phe	Ser	Gln	Asp	Val	Ala	Pro	Gln	Tyr	Val	Asp
	210					215					220				
Ile	Ser	Ala	Gly	Gly	Gly	Lys									
225					230										

<210> 348
 <211> 514
 <212> PRT
 <213> Escherichia coli

<400> 348															
Met	Lys	Ile	Arg	Ser	Gln	Val	Gly	Met	Val	Leu	Asn	Leu	Asp	Lys	Cys
1				5					10					15	
Ile	Gly	Cys	His	Thr	Cys	Ser	Val	Thr	Cys	Lys	Asn	Val	Trp	Thr	Gly
			20					25					30		
Arg	Glu	Gly	Met	Glu	Tyr	Ala	Trp	Phe	Asn	Asn	Val	Glu	Thr	Lys	Pro
		35					40					45			
Gly	Ile	Gly	Tyr	Pro	Lys	Asn	Trp	Glu	Asp	Gln	Glu	Glu	Trp	Gln	Gly
	50					55					60				
Gly	Trp	Val	Arg	Asp	Val	Asn	Gly	Lys	Ile	Arg	Pro	Arg	Leu	Gly	Asn
65					70				75						80
Lys	Met	Gly	Val	Ile	Thr	Lys	Ile	Phe	Ala	Asn	Pro	Val	Val	Pro	Gln
				85				90						95	
Ile	Asp	Asp	Tyr	Tyr	Glu	Pro	Phe	Thr	Phe	Asp	Tyr	Glu	His	Leu	His
			100				105						110		
Ser	Ala	Pro	Glu	Gly	Lys	His	Ile	Pro	Thr	Ala	Arg	Pro	Arg	Ser	Leu
		115					120					125			
Ile	Asp	Gly	Lys	Arg	Met	Asp	Lys	Val	Ile	Trp	Gly	Pro	Asn	Trp	Glu
	130					135					140				
Glu	Leu	Leu	Gly	Gly	Glu	Phe	Glu	Lys	Arg	Ala	Arg	Asp	Arg	Asn	Phe
145					150				155						160
Glu	Ala	Met	Gln	Lys	Glu	Met	Tyr	Gly	Gln	Phe	Glu	Asn	Thr	Phe	Met
				165				170						175	
Met	Tyr	Leu	Pro	Arg	Leu	Cys	Glu	His	Cys	Leu	Asn	Pro	Ser	Cys	Val
			180				185						190		
Ala	Thr	Cys	Pro	Ser	Gly	Ala	Ile	Tyr	Lys	Arg	Glu	Glu	Asp	Gly	Ile
		195					200					205			
Val	Leu	Ile	Asp	Gln	Asp	Lys	Cys	Arg	Gly	Trp	Arg	Leu	Cys	Ile	Ser
	210					215					220				
Gly	Cys	Pro	Tyr	Lys	Lys	Ile	Tyr	Phe	Asn	Trp	Lys	Ser	Gly	Lys	Ser
225					230				235						240
Glu	Lys	Cys	Ile	Phe	Cys	Tyr	Pro	Arg	Ile	Glu	Ser	Gly	Gln	Pro	Thr
				245				250						255	
Val	Cys	Ser	Glu	Thr	Cys	Val	Gly	Arg	Ile	Arg	Tyr	Leu	Gly	Val	Leu
			260				265						270		
Leu	Tyr	Asp	Ala	Asp	Arg	Ile	Glu	Glu	Ala	Ala	Ser	Thr	Glu	Arg	Glu
		275					280					285			
Val	Asp	Leu	Tyr	Glu	Arg	Gln	Cys	Glu	Val	Phe	Leu	Asp	Pro	His	Asp
	290					295				300					
Pro	Ser	Val	Ile	Glu	Glu	Ala	Leu	Lys	Gln	Gly	Ile	Pro	Gln	Asn	Val
305					310				315						320
Ile	Asp	Ala	Ala	Gln	Arg	Ser	Pro	Val	Tyr	Lys	Met	Ala	Met	Asp	Trp

Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser
 1105 1110 1115 1120
 Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu
 1125 1130 1135
 Val Phe Asn Ala Asn Gly Ala Leu Thr Ala Arg Ala Val Val Ser Gln
 1140 1145 1150
 Arg Val Pro Pro Gly Met Thr Met Met Tyr His Ala Gln Glu Arg Ile
 1155 1160 1165
 Met Asn Ile Pro Gly Ser Glu Val Thr Gly Met Arg Gly Gly Ile His
 1170 1175 1180
 Asn Ser Val Thr Arg Val Cys Pro Lys Pro Thr His Met Ile Gly Gly
 1185 1190 1195 1200
 Tyr Ala Gln Leu Ala Trp Gly Phe Asn Tyr Tyr Gly Thr Val Gly Ser
 1205 1210 1215
 Asn Arg Asp Glu Phe Ile Met Ile Arg Lys Met Lys Asn Val Asn Trp
 1220 1225 1230
 Leu Asp Asp Glu Gly Arg Asp Gln Val Gln Glu Ala Lys Lys
 1235 1240 1245

<210> 350
 <211> 165
 <212> PRT
 <213> Escherichia coli

<400> 350
 Met Asp Leu Ser Gln Leu Thr Pro Arg Arg Pro Tyr Leu Leu Arg Ala
 1 5 10 15
 Phe Tyr Glu Trp Leu Leu Asp Asn Gln Leu Thr Pro His Leu Val Val
 20 25 30
 Asp Val Thr Leu Pro Gly Val Gln Val Pro Met Glu Tyr Ala Arg Asp
 35 40 45
 Gly Gln Ile Val Leu Asn Ile Ala Pro Arg Ala Val Gly Asn Leu Glu
 50 55 60
 Leu Ala Asn Asp Glu Val Arg Phe Asn Ala Arg Phe Gly Gly Ile Pro
 65 70 75 80
 Arg Gln Val Ser Val Pro Leu Ala Ala Val Leu Ala Ile Tyr Ala Arg
 85 90 95
 Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu
 100 105 110
 Asp Thr Ser Ile Met Asn Asp Glu Ala Ser Ala Asp Asn Glu Thr
 115 120 125
 Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr
 130 135 140
 His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala
 145 150 155 160
 Leu Arg Val Val Lys
 165

<210> 351
 <211> 212
 <212> PRT
 <213> Escherichia coli

<400> 351
 Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly

1	5	10	15
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys			
	20	25	30
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln			
	35	40	45
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp			
	50	55	60
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp			
65	70	75	80
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg			
	85	90	95
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr			
	100	105	110
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala			
	115	120	125
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly			
	130	135	140
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr			
145	150	155	160
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser			
	165	170	175
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu			
	180	185	190
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg			
	195	200	205
Leu Gly Arg Ser			
210			

<210> 352
 <211> 505
 <212> PRT
 <213> Escherichia coli

<400> 352
Met Ser Glu Gln His Ala Gln Gly Ala Asp Ala Val Val Asp Leu Asn
1 5 10 15
Asn Glu Leu Lys Thr Arg Arg Glu Lys Leu Ala Asn Leu Arg Glu Gln
20 25 30
Gly Ile Ala Phe Pro Asn Asp Phe Arg Arg Asp His Thr Ser Asp Gln
35 40 45
Leu His Ala Glu Phe Asp Gly Lys Glu Asn Glu Glu Leu Glu Ala Leu
50 55 60
Asn Ile Glu Val Ala Val Ala Gly Arg Met Met Thr Arg Arg Ile Met
65 70 75 80
Gly Lys Ala Ser Phe Val Thr Leu Gln Asp Val Gly Gly Arg Ile Gln
85 90 95
Leu Tyr Val Ala Arg Asp Asp Leu Pro Glu Gly Val Tyr Asn Glu Gln
100 105 110
Phe Lys Lys Trp Asp Leu Gly Asp Ile Leu Gly Ala Lys Gly Lys Leu
115 120 125
Phe Lys Thr Lys Thr Gly Glu Leu Ser Ile His Cys Thr Glu Leu Arg
130 135 140
Leu Leu Thr Lys Ala Leu Arg Pro Leu Pro Asp Lys Phe His Gly Leu
145 150 155 160
Gln Asp Gln Glu Ala Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Ser
165 170 175

530 535 540
 Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu
 545 550 555 560
 Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro
 565 570 575
 Ile

<210> 355
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 355
 Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
 1 5 10 15
 Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
 20 25 30
 Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
 35 40 45
 Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 50 55 60
 His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 65 70 75 80
 Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 85 90 95
 Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 100 105 110
 Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125
 Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140
 Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160
 Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 225 230 235

<210> 356
 <211> 298
 <212> PRT
 <213> Escherichia coli

<400> 356
 Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1 5 10 15
 Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
 20 25 30

0074660-121900

Gly	Lys	Glu	Thr	Cys	Arg	Thr	Asn	Ala	Ala	Thr	Val	Ala	Val	Ile	Gln
145					150					155					160
Asp	Ala	Leu	Lys	Ser	Cys	Gly	Leu	Pro	Ala	Gly	Ala	Val	Gln	Ala	Ile
				165					170						175
Asp	Asn	Pro	Asp	Arg	Ala	Leu	Val	Ser	Glu	Met	Leu	Arg	Met	Asp	Lys
			180					185					190		
Tyr	Ile	Asp	Met	Leu	Ile	Pro	Arg	Gly	Gly	Ala	Gly	Leu	His	Lys	Leu
		195					200					205			
Cys	Arg	Glu	Gln	Ser	Thr	Ile	Pro	Val	Ile	Thr	Gly	Gly	Ile	Gly	Val
	210					215					220				
Cys	His	Ile	Tyr	Val	Asp	Glu	Ser	Val	Glu	Ile	Ala	Glu	Ala	Leu	Lys
225					230					235					240
Val	Ile	Val	Asn	Ala	Lys	Thr	Gln	Arg	Pro	Ser	Thr	Cys	Asn	Thr	Val
			245						250						255
Glu	Thr	Leu	Leu	Val	Asn	Lys	Asn	Ile	Ala	Asp	Ser	Phe	Leu	Pro	Ala
		260					265						270		
Leu	Ser	Lys	Gln	Met	Ala	Glu	Ser	Gly	Val	Thr	Leu	His	Ala	Asp	Ala
		275					280					285			
Ala	Ala	Leu	Ala	Gln	Leu	Gln	Ala	Gly	Pro	Ala	Lys	Val	Val	Ala	Val
	290					295					300				
Lys	Ala	Glu	Glu	Tyr	Asp	Asp	Glu	Phe	Leu	Ser	Leu	Asp	Leu	Asn	Val
305					310					315					320
Lys	Ile	Val	Ser	Asp	Leu	Asp	Asp	Ala	Ile	Ala	His	Ile	Arg	Glu	His
			325						330					335	
Gly	Thr	Gln	His	Ser	Asp	Ala	Ile	Leu	Thr	Arg	Asp	Met	Arg	Asn	Ala
		340						345					350		
Gln	Arg	Phe	Val	Asn	Glu	Val	Asp	Ser	Ser	Ala	Val	Tyr	Val	Asn	Ala
		355					360					365			
Ser	Thr	Arg	Phe	Thr	Asp	Gly	Gly	Gln	Phe	Gly	Leu	Gly	Ala	Glu	Val
	370					375					380				
Ala	Val	Ser	Thr	Gln	Lys	Leu	His	Ala	Arg	Gly	Pro	Met	Gly	Leu	Glu
385					390					395					400
Ala	Leu	Thr	Thr	Tyr	Lys	Trp	Ile	Gly	Ile	Gly	Asp	Tyr	Thr	Ile	Arg
				405					410					415	
Ala															

<210> 359
 <211> 186
 <212> PRT
 <213> Escherichia coli

<400> 359

Met	Met	Thr	Arg	Gln	Ala	Ser	Met	Lys	Gly	Phe	Pro	Ile	Ala	His	Ile
1				5					10					15	
Phe	His	Pro	Ser	Ile	Pro	Pro	Met	His	Ala	Val	Val	Asn	Asn	His	Asn
		20					25						30		
Arg	Asn	Ile	Asp	Tyr	Trp	Thr	Val	Lys	Arg	Lys	Phe	Ala	Glu	Ile	Val
	35					40						45			
Ser	Thr	Asn	Asp	Val	Asn	Lys	Ile	Tyr	Ser	Ile	Ser	Asn	Glu	Leu	Arg
	50				55					60					
Arg	Val	Leu	Ser	Ala	Ile	Thr	Ala	Leu	Asn	Phe	Tyr	His	Gly	Asp	Val
65					70				75						80
Pro	Ser	Val	Met	Ile	Arg	Ile	Gln	Pro	Glu	Asn	Met	Ser	Pro	Phe	Ile
			85					90					95		
Ile	Asp	Ile	Ser	Thr	Gly	Glu	His	Asp	Asp	Tyr	Ile	Ile	Gln	Thr	Leu

Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu
 305 310 315 320
 Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn
 325 330 335
 Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu
 340 345 350
 Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn
 355 360 365
 Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp
 370 375 380
 Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile
 385 390 395

<210> 361
 <211> 315
 <212> PRT
 <213> Escherichia coli

<400> 361
 Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe
 1 5 10 15
 Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr
 20 25 30
 Leu Ile Pro Leu Arg Gln Gln Ala Leu Lys Val Ile Asn Gln Leu
 35 40 45
 Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu
 50 55 60
 Ala Phe Leu Asp Asn Leu Ala Ser Asn Leu Leu Ala Ile Leu His Tyr
 65 70 75 80
 Ser Ala Val Ser Ile Thr Val Ile Leu Leu Cys Asn Ile Ala Ala Leu
 85 90 95
 Met Trp Leu Glu Arg Gly Leu Pro Trp Arg Asn His His Gln Gln Glu
 100 105 110
 Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys
 115 120 125
 Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe
 130 135 140
 Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu
 145 150 155 160
 Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln
 165 170 175
 Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val
 180 185 190
 Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro
 195 200 205
 Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu
 210 215 220
 Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala
 225 230 235 240
 Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile
 245 250 255
 Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly
 260 265 270
 Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly
 275 280 285
 Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu

290 295 300
 Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala
 305 310 315

<210> 362
 <211> 96
 <212> PRT
 <213> Escherichia coli

<400> 362
 Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
 1 5 10 15
 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
 20 25 30
 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
 35 40 45
 Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
 50 55 60
 Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
 65 70 75 80
 Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
 85 90 95

<210> 363
 <211> 562
 <212> PRT
 <213> Escherichia coli

<400> 363
 Met Ala Ser Ser Gly Thr Thr Ser Thr Arg Lys Arg Phe Thr Gly Ala
 1 5 10 15
 Glu Phe Ile Val His Phe Leu Glu Gln Gln Gly Ile Lys Ile Val Thr
 20 25 30
 Gly Ile Pro Gly Gly Ser Ile Leu Pro Val Tyr Asp Ala Leu Ser Gln
 35 40 45
 Ser Thr Gln Ile Arg His Ile Leu Ala Arg His Glu Gln Gly Ala Gly
 50 55 60
 Phe Ile Ala Gln Gly Met Ala Arg Thr Asp Gly Lys Pro Ala Val Cys
 65 70 75 80
 Met Ala Cys Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Ala Ile Ala
 85 90 95
 Asp Ala Arg Leu Asp Ser Ile Pro Leu Ile Cys Ile Thr Gly Gln Val
 100 105 110
 Pro Ala Ser Met Ile Gly Thr Asp Ala Phe Gln Glu Val Asp Thr Tyr
 115 120 125
 Gly Ile Ser Ile Pro Ile Thr Lys His Asn Tyr Leu Val Arg His Ile
 130 135 140
 Glu Glu Leu Pro Gln Val Met Ser Asp Ala Phe Arg Ile Ala Gln Ser
 145 150 155 160
 Gly Arg Pro Gly Pro Val Trp Ile Asp Ile Pro Lys Asp Val Gln Thr
 165 170 175
 Ala Val Phe Glu Ile Glu Thr Gln Pro Ala Met Ala Glu Lys Ala Ala
 180 185 190
 Ala Pro Ala Phe Ser Glu Glu Ser Ile Arg Asp Ala Ala Ala Met Ile
 195 200 205

20

25

30

<210> 365

<211> 338

<212> PRT

<213> Escherichia coli

<400> 365

Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
 245 250 255
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
 260 265 270
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
 275 280 285
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
 290 295 300
 Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 366

<211> 157

<212> PRT
<213> Escherichia coli

<400> 366

Met	Val	Tyr	Ile	Ile	Ile	Val	Ser	His	Gly	His	Glu	Asp	Tyr	Ile	Lys
1				5					10					15	
Lys	Leu	Leu	Glu	Asn	Leu	Asn	Ala	Asp	Asp	Glu	His	Tyr	Lys	Ile	Ile
			20					25					30		
Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His
		35					40					45			
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His
	50					55					60				
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala
65					70					75				80	
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His
				85					90					95	
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala
			100					105					110		
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp
		115					120					125			
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe
	130					135					140				
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile			
145					150					155					

<210> 367
<211> 372
<212> PRT
<213> Escherichia coli

<400> 367

Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly
1				5					10					15	
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys
			20					25					30		
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys
		35					40					45			
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly
	50					55					60				
Ser	Trp	Leu	Lys	Arg	Leu	His	Phe	Glu	Tyr	Val	Val	Cys	Lys	Lys	Leu
65					70					75					80
Ser	Lys	Glu	Leu	Asn	Ala	Thr	His	Trp	Ile	Cys	Leu	His	Asp	Ile	Thr
				85					90					95	
Ala	Asn	Val	Val	Thr	Lys	Lys	Arg	Tyr	Val	Tyr	Cys	His	Asn	Pro	Ala
			100					105					110		
Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser
		115					120					125			
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile
	130					135					140				
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys
145					150					155				160	
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu
				165					170					175	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe
		180						185					190		
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg

<210> 369
 <211> 330
 <212> PRT
 <213> Escherichia coli

<400> 369

Met	Tyr	Phe	Leu	Asn	Asp	Leu	Asn	Phe	Ser	Arg	Arg	Asp	Ala	Gly	Phe
1				5					10					15	
Lys	Ala	Arg	Lys	Asp	Ala	Leu	Asp	Ile	Ala	Ser	Asp	Tyr	Glu	Asn	Ile
			20					25					30		
Ser	Val	Val	Asn	Ile	Pro	Leu	Trp	Gly	Gly	Val	Val	Gln	Arg	Ile	Ile
		35					40					45			
Ser	Ser	Val	Lys	Leu	Ser	Thr	Phe	Leu	Cys	Gly	Leu	Glu	Asn	Lys	Asp
	50					55					60				
Val	Leu	Ile	Phe	Asn	Phe	Pro	Met	Ala	Lys	Pro	Phe	Trp	His	Ile	Leu
65					70					75					80
Ser	Phe	Phe	His	Arg	Leu	Leu	Lys	Phe	Arg	Ile	Val	Pro	Leu	Ile	His
				85					90					95	
Asp	Ile	Asp	Glu	Leu	Arg	Gly	Gly	Gly	Gly	Ser	Asp	Ser	Val	Arg	Leu
			100					105					110		
Ala	Thr	Cys	Asp	Met	Val	Ile	Ser	His	Asn	Pro	Gln	Met	Thr	Lys	Tyr
		115					120					125			
Leu	Ser	Lys	Tyr	Met	Ser	Gln	Asp	Lys	Ile	Lys	Asp	Ile	Lys	Ile	Phe
	130					135					140				
Asp	Tyr	Leu	Val	Ser	Ser	Asp	Val	Glu	His	Arg	Asp	Val	Thr	Asp	Lys
145					150					155					160
Gln	Arg	Gly	Val	Ile	Tyr	Ala	Gly	Asn	Leu	Ser	Arg	His	Lys	Cys	Ser
				165				170						175	
Phe	Ile	Tyr	Thr	Glu	Gly	Cys	Asp	Phe	Thr	Leu	Phe	Gly	Val	Asn	Tyr
			180					185					190		
Glu	Asn	Lys	Asp	Asn	Pro	Lys	Tyr	Leu	Gly	Ser	Phe	Asp	Ala	Gln	Ser
		195					200					205			
Pro	Glu	Lys	Ile	Asn	Leu	Pro	Gly	Met	Gln	Phe	Gly	Leu	Ile	Trp	Asp
	210				215						220				
Gly	Asp	Ser	Val	Glu	Thr	Cys	Ser	Gly	Ala	Phe	Gly	Asp	Tyr	Leu	Lys
225					230				235						240
Phe	Asn	Asn	Pro	His	Lys	Thr	Ser	Leu	Tyr	Leu	Ser	Met	Glu	Leu	Pro
				245					250					255	
Val	Phe	Ile	Trp	Asp	Lys	Ala	Ala	Leu	Ala	Asp	Phe	Ile	Val	Asp	Asn
			260					265					270		
Arg	Ile	Gly	Tyr	Ala	Val	Gly	Ser	Ile	Lys	Glu	Met	Gln	Glu	Ile	Val
		275					280					285			
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys
	290					295					300				
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu
305					310					315					320
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg						
				325					330						

<210> 370
 <211> 388
 <212> PRT
 <213> Escherichia coli

<400> 370

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
1 5 10 15
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
20 25 30
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
35 40 45
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
50 55 60
Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
65 70 75 80
Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
85 90 95
Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
100 105 110
Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
115 120 125
Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
130 135 140
Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
145 150 155 160
Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
165 170 175
Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
180 185 190
Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
195 200 205
Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
210 215 220
Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
225 230 235 240
Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
245 250 255
Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
260 265 270
Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
275 280 285
Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
290 295 300
Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
305 310 315 320
Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
325 330 335
Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
340 345 350
Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
355 360 365
Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
370 375 380
Gln Lys Ile Lys
385

<210> 371

<211> 367

<212> PRT

<213> Escherichia coli

[illegible]

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<210> 372
<211> 230
<212> PRT
<213> Escherichia coli
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Met Thr Ser Ser Ile Thr Asn Glu Ile Met Gln Leu Tyr Thr Asp Arg

[illegible]

<400> 374

415

145 150 155 160
 Cys Gln Leu Tyr Gln Arg Ser Cys Asp Val Phe Leu Gly Leu Pro Phe
 165 170 175
 Asn Ile Ala Ser Tyr Ala Leu Leu Val His Met Met Ala Gln Gln Cys
 180 185 190
 Asp Leu Glu Val Gly Asp Phe Val Trp Thr Gly Gly Asp Thr His Leu
 195 200 205
 Tyr Ser Asn His Met Asp Gln Thr His Leu Gln Leu Ser Arg Glu Pro
 210 215 220
 Arg Pro Leu Pro Lys Leu Ile Ile Lys Arg Lys Pro Glu Ser Ile Phe
 225 230 235 240
 Asp Tyr Arg Phe Glu Asp Phe Glu Ile Glu Gly Tyr Asp Pro His Pro
 245 250 255
 Gly Ile Lys Ala Pro Val Ala Ile
 260

<210> 375
 <211> 291
 <212> PRT
 <213> Escherichia coli

<400> 375
 Met Thr Ser Ser Tyr Leu His Phe Pro Glu Phe Asp Pro Val Ile Phe
 1 5 10 15
 Ser Ile Gly Pro Val Ala Leu His Trp Tyr Gly Leu Met Tyr Leu Val
 20 25 30
 Gly Phe Ile Phe Ala Met Trp Leu Ala Thr Arg Arg Ala Asn Arg Pro
 35 40 45
 Gly Ser Gly Trp Thr Lys Asn Glu Val Glu Asn Leu Leu Tyr Ala Gly
 50 55 60
 Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr
 65 70 75 80
 Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp
 85 90 95
 Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val
 100 105 110
 Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser
 115 120 125
 Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu
 130 135 140
 Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe
 145 150 155 160
 Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu
 165 170 175
 Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val
 180 185 190
 Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val
 195 200 205
 Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met
 210 215 220
 Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile
 225 230 235 240
 Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp
 245 250 255
 Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val
 260 265 270

Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln
 275 280 285
 His Val Ser
 290

<210> 376
 <211> 241
 <212> PRT
 <213> Escherichia coli

<400> 376
 Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
 1 5 10 15
 Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
 20 25 30
 Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
 35 40 45
 Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
 50 55 60
 Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
 65 70 75 80
 Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
 85 90 95
 Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
 100 105 110
 Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
 115 120 125
 Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
 130 135 140
 Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
 145 150 155 160
 Asp Lys Lys Val Asp Gln Glu Tyr Glu Gly Ile Val Arg Gln Leu Met
 165 170 175
 Thr Tyr Met Met Glu Asp Ser Arg Thr Ile Pro Ser Val Leu Thr Ala
 180 185 190
 Leu Phe Cys Ala Arg Ser Ile Glu Arg Ile Gly Asp Arg Cys Gln Asn
 195 200 205
 Ile Cys Glu Phe Ile Phe Tyr Tyr Val Lys Gly Gln Asp Phe Arg His
 210 215 220
 Val Gly Gly Asp Glu Leu Asp Lys Leu Leu Ala Gly Lys Asp Ser Asp
 225 230 235 240
 Lys

<210> 377
 <211> 257
 <212> PRT
 <213> Escherichia coli

<400> 377
 Met Ser Met Val Glu Thr Ala Pro Ser Lys Ile Gln Val Arg Asn Leu
 1 5 10 15
 Asn Phe Tyr Tyr Gly Lys Phe His Ala Leu Lys Asn Ile Asn Leu Asp
 20 25 30
 Ile Ala Lys Asn Gln Val Thr Ala Phe Ile Gly Pro Ser Gly Cys Gly

Ala	Leu	Leu	Gln	Val	Pro	Ile	Val	Ile	Arg	Thr	Thr	Glu	Asn	Met	Leu
				165					170					175	
Lys	Leu	Val	Pro	Tyr	Ser	Leu	Arg	Glu	Ala	Ala	Tyr	Ala	Leu	Gly	Thr
			180					185					190		
Pro	Lys	Trp	Lys	Met	Ile	Ser	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Val	Ser
	195						200					205			
Gly	Ile	Met	Thr	Gly	Ile	Leu	Leu	Ala	Ile	Ala	Arg	Ile	Ala	Gly	Glu
	210					215					220				
Thr	Ala	Pro	Leu	Leu	Phe	Thr	Ala	Leu	Ser	Asn	Gln	Phe	Trp	Ser	Thr
225					230					235					240
Asp	Met	Met	Gln	Pro	Ile	Ala	Asn	Leu	Pro	Val	Thr	Ile	Phe	Lys	Phe
				245					250					255	
Ala	Met	Ser	Pro	Phe	Ala	Glu	Trp	Gln	Gln	Leu	Ala	Trp	Ala	Gly	Val
			260					265					270		
Leu	Ile	Ile	Thr	Leu	Cys	Val	Leu	Leu	Leu	Asn	Ile	Leu	Ala	Arg	Val
	275						280					285			
Val	Phe	Ala	Lys	Asn	Lys	His	Gly								
	290						295								

<210> 379
 <211> 319
 <212> PRT
 <213> Escherichia coli

<400> 379

Met	Ala	Ala	Thr	Lys	Pro	Ala	Phe	Asn	Pro	Pro	Gly	Lys	Lys	Gly	Asp
1				5					10					15	
Ile	Ile	Phe	Ser	Val	Leu	Val	Lys	Leu	Ala	Ala	Leu	Ile	Val	Leu	Leu
			20					25					30		
Met	Leu	Gly	Gly	Ile	Ile	Val	Ser	Leu	Ile	Ile	Ser	Ser	Trp	Pro	Ser
	35						40					45			
Ile	Gln	Lys	Phe	Gly	Leu	Ala	Phe	Leu	Trp	Thr	Lys	Glu	Trp	Asp	Ala
	50					55					60				
Pro	Asn	Asp	Ile	Tyr	Gly	Ala	Leu	Val	Pro	Ile	Tyr	Gly	Thr	Leu	Val
65					70					75					80
Thr	Ser	Phe	Ile	Ala	Leu	Leu	Ile	Ala	Val	Pro	Val	Ser	Phe	Gly	Ile
			85						90					95	
Ala	Leu	Phe	Leu	Thr	Glu	Leu	Ala	Pro	Gly	Trp	Leu	Lys	Arg	Pro	Leu
			100					105					110		
Gly	Ile	Ala	Ile	Glu	Leu	Leu	Ala	Ala	Ile	Pro	Ser	Ile	Val	Tyr	Gly
	115						120					125			
Met	Trp	Gly	Leu	Phe	Ile	Phe	Ala	Pro	Leu	Phe	Ala	Val	Tyr	Phe	Gln
	130					135					140				
Glu	Pro	Val	Gly	Asn	Ile	Met	Ser	Asn	Ile	Pro	Ile	Val	Gly	Ala	Leu
145					150					155					160
Phe	Ser	Gly	Pro	Ala	Phe	Gly	Ile	Gly	Ile	Leu	Ala	Ala	Gly	Val	Ile
				165					170					175	
Leu	Ala	Ile	Met	Ile	Ile	Pro	Tyr	Ile	Ala	Ala	Val	Met	Arg	Asp	Val
			180					185					190		
Phe	Glu	Gln	Thr	Pro	Val	Met	Met	Lys	Glu	Ser	Ala	Tyr	Gly	Ile	Gly
		195					200					205			
Cys	Thr	Thr	Trp	Glu	Val	Ile	Trp	Arg	Ile	Val	Leu	Pro	Phe	Thr	Lys
	210					215					220				
Asn	Gly	Val	Ile	Gly	Gly	Ile	Met	Leu	Gly	Leu	Gly	Arg	Ala	Leu	Gly
225					230					235					240
Glu	Thr	Met	Ala	Val	Thr	Phe	Ile	Ile	Gly	Asn	Thr	Tyr	Gln	Leu	Asp

Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn
 325 330 335
 Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr
 340 345

<210> 381
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 381
 Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu
 1 5 10 15
 Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr
 20 25 30
 Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
 35 40 45
 Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
 50 55 60
 Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
 65 70 75 80
 Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
 85 90 95
 Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu
 100 105 110
 Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
 115 120 125
 Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe
 130 135 140
 Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala
 145 150 155 160
 Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln
 165 170 175
 Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp
 180 185 190
 Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser
 195 200 205
 Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala
 210 215 220
 Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys
 225 230 235

<210> 382
 <211> 181
 <212> PRT
 <213> Escherichia coli

<400> 382
 Met Gln Ala Lys Ile Ala Ala Ser Asn Thr Gly Glu Leu Asp Ala Leu
 1 5 10 15
 Gln Gln Leu Gly Phe Ser Leu Val Glu Gly Glu Val Asp Leu Ala Leu
 20 25 30
 Pro Val Asn Asn Ala Ser Asp Ser Gly Ala Val Val Ala Gln Glu Thr
 35 40 45
 Asp Ile Pro Ala Leu Arg Gln Leu Ala Ser Ala Ala Phe Ala Gln Ser

Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala
 260 265 270
 Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln
 275 280 285
 Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser
 290 295 300
 Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His
 305 310 315 320
 Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe
 325 330 335
 His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg
 340 345 350
 Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile
 355 360 365
 Ala Thr Leu Leu Asn Tyr Phe Ser
 370 375

<210> 384
 <211> 416
 <212> PRT
 <213> Escherichia coli

<400> 384
 Met Ser Leu Ala Lys Ala Ser Leu Trp Thr Ala Ala Ser Thr Leu Val
 1 5 10 15
 Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
 20 25 30
 Gly Pro Ala Gly Leu Gly Leu Ala Ala Asn Phe Arg Gln Leu Ile Thr
 35 40 45
 Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
 50 55 60
 Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
 65 70 75 80
 Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
 85 90 95
 Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
 100 105 110
 Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
 115 120 125
 Ile Ala Trp Gly Asn Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
 130 135 140
 Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
 145 150 155 160
 Leu Ala Tyr Tyr Val Ser Tyr Arg Leu Gly Gly Tyr Glu Gly Ala Leu
 165 170 175
 Leu Gly Leu Ala Leu Ile Pro Ala Leu Val Val Ile Pro Ala Ala Ile
 180 185 190
 Met Leu Ile Lys Arg Gly Val Ile Pro Leu Ser Tyr Leu Lys Pro Ser
 195 200 205
 Trp Asp Asn Gly Leu Ala Gly Gln Leu Ser Lys Phe Thr Leu Met Ala
 210 215 220
 Leu Ile Thr Ser Val Thr Leu Pro Val Ala Tyr Ile Met Met Arg Lys
 225 230 235 240
 Leu Leu Ala Ala Gln Tyr Ser Trp Asp Glu Val Gly Ile Trp Gln Gly
 245 250 255
 Val Ser Ser Ile Ser Asp Ala Tyr Leu Gln Phe Ile Thr Ala Ser Phe

Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
165 170 175
Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp
180 185 190
Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala
195 200

<210> 389
<211> 182
<212> PRT
<213> Escherichia coli

<400> 389
Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
1 5 10 15
Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
20 25 30
Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
35 40 45
Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
50 55 60
Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
65 70 75 80
Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
85 90 95
Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
100 105 110
Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
115 120 125
Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
130 135 140
Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
145 150 155 160
Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
165 170 175
Ser Lys Val Trp Glu Trp
180

<210> 390
<211> 91
<212> PRT
<213> Escherichia coli

<400> 390
Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
1 5 10 15
Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
20 25 30
Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
35 40 45
Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
50 55 60
Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Glu Ala Ala Glu Leu
65 70 75 80
Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg

<210> 391
 <211> 702
 <212> PRT
 <213> Escherichia coli

<400> 391

Met	Tyr	Leu	Phe	Glu	Ser	Leu	Asn	Gln	Leu	Ile	Gln	Thr	Tyr	Leu	Pro
1				5					10					15	
Glu	Asp	Gln	Ile	Lys	Arg	Leu	Arg	Gln	Ala	Tyr	Leu	Val	Ala	Arg	Asp
			20					25					30		
Ala	His	Glu	Gly	Gln	Thr	Arg	Ser	Ser	Gly	Glu	Pro	Tyr	Ile	Thr	His
		35				40						45			
Pro	Val	Ala	Val	Ala	Cys	Ile	Leu	Ala	Glu	Met	Lys	Leu	Asp	Tyr	Glu
	50					55					60				
Thr	Leu	Met	Ala	Ala	Leu	Leu	His	Asp	Val	Ile	Glu	Asp	Thr	Pro	Ala
65					70					75					80
Thr	Tyr	Gln	Asp	Met	Glu	Gln	Leu	Phe	Gly	Lys	Ser	Val	Ala	Glu	Leu
			85						90					95	
Val	Glu	Gly	Val	Ser	Lys	Leu	Asp	Lys	Leu	Lys	Phe	Arg	Asp	Lys	Lys
			100					105					110		
Glu	Ala	Gln	Ala	Glu	Asn	Phe	Arg	Lys	Met	Ile	Met	Ala	Met	Val	Gln
		115					120					125			
Asp	Ile	Arg	Val	Ile	Leu	Ile	Lys	Leu	Ala	Asp	Arg	Thr	His	Asn	Met
	130					135					140				
Arg	Thr	Leu	Gly	Ser	Leu	Arg	Pro	Asp	Lys	Arg	Arg	Arg	Ile	Ala	Arg
145					150					155					160
Glu	Thr	Leu	Glu	Ile	Tyr	Ser	Pro	Leu	Ala	His	Arg	Leu	Gly	Ile	His
			165						170					175	
His	Ile	Lys	Thr	Glu	Leu	Glu	Glu	Leu	Gly	Phe	Glu	Ala	Leu	Tyr	Pro
			180					185					190		
Asn	Arg	Tyr	Arg	Val	Ile	Lys	Glu	Val	Val	Lys	Ala	Ala	Arg	Gly	Asn
		195					200					205			
Arg	Lys	Glu	Met	Ile	Gln	Lys	Ile	Leu	Ser	Glu	Ile	Glu	Gly	Arg	Leu
	210					215					220				
Gln	Glu	Ala	Gly	Ile	Pro	Cys	Arg	Val	Ser	Gly	Arg	Glu	Lys	His	Leu
225					230					235					240
Tyr	Ser	Ile	Tyr	Cys	Lys	Met	Val	Leu	Lys	Glu	Gln	Arg	Phe	His	Ser
			245						250					255	
Ile	Met	Asp	Ile	Tyr	Ala	Phe	Arg	Val	Ile	Val	Asn	Asp	Ser	Asp	Thr
		260						265					270		
Cys	Tyr	Arg	Val	Leu	Gly	Gln	Met	His	Ser	Leu	Tyr	Lys	Pro	Arg	Pro
		275					280					285			
Gly	Arg	Val	Lys	Asp	Tyr	Ile	Ala	Ile	Pro	Lys	Ala	Asn	Gly	Tyr	Gln
	290					295					300				
Ser	Leu	His	Thr	Ser	Met	Ile	Gly	Pro	His	Gly	Val	Pro	Val	Glu	Val
305					310					315					320
Gln	Ile	Arg	Thr	Glu	Asp	Met	Asp	Gln	Met	Ala	Glu	Met	Gly	Val	Ala
			325						330					335	
Ala	His	Trp	Ala	Tyr	Lys	Glu	His	Gly	Glu	Thr	Ser	Thr	Thr	Ala	Gln
			340					345					350		
Ile	Arg	Ala	Gln	Arg	Trp	Met	Gln	Ser	Leu	Leu	Glu	Leu	Gln	Gln	Ser
		355					360					365			
Ala	Gly	Ser	Ser	Phe	Glu	Phe	Ile	Glu	Ser	Val	Lys	Ser	Asp	Leu	Phe
	370					375						380			

65		70		75		80									
Asp	Ala	Val	Ala	His	Leu	Lys	Gly	Gln	Gly	Met	Gln	Ile	Leu	Ala	Thr
			85						90					95	
His	Leu	Ser	Asp	Asn	Ala	Val	Asp	Phe	Arg	Glu	Ile	Asp	Tyr	Thr	Arg
			100					105					110		
Pro	Thr	Cys	Ile	Leu	Met	Gly	Gln	Glu	Lys	Thr	Gly	Ile	Thr	Gln	Glu
		115					120					125			
Ala	Leu	Ala	Leu	Ala	Asp	Gln	Asp	Ile	Ile	Ile	Pro	Met	Ile	Gly	Met
	130					135					140				
Val	Gln	Ser	Leu	Asn	Val	Ser	Val	Ala	Ser	Ala	Leu	Ile	Leu	Tyr	Glu
145				150						155					160
Ala	Gln	Arg	Gln	Arg	Gln	Asn	Ala	Gly	Met	Tyr	Leu	Arg	Glu	Asn	Ser
				165					170					175	
Met	Leu	Pro	Glu	Ala	Glu	Gln	Gln	Arg	Leu	Leu	Phe	Glu	Gly	Gly	Tyr
			180					185					190		
Pro	Val	Leu	Ala	Lys	Val	Ala	Lys	Arg	Lys	Gly	Leu	Pro	Tyr	Pro	His
		195					200					205			
Val	Asn	Gln	Gln	Gly	Glu	Ile	Glu	Ala	Asp	Ala	Asp	Trp	Trp	Ala	Thr
	210					215					220				
Met	Gln	Ala	Ala	Gly											
225															

<210> 393
 <211> 693
 <212> PRT
 <213> Escherichia coli

<400> 393

Met	Lys	Gly	Arg	Leu	Leu	Asp	Ala	Val	Pro	Leu	Ser	Ser	Leu	Thr	Gly
1				5					10				15		
Val	Gly	Ala	Ala	Leu	Ser	Asn	Lys	Leu	Ala	Lys	Ile	Asn	Leu	His	Thr
			20					25					30		
Val	Gln	Asp	Leu	Leu	Leu	His	Leu	Pro	Leu	Arg	Tyr	Glu	Asp	Arg	Thr
		35				40						45			
His	Leu	Tyr	Pro	Ile	Gly	Glu	Leu	Leu	Pro	Gly	Val	Tyr	Ala	Thr	Val
	50				55					60					
Glu	Gly	Glu	Val	Leu	Asn	Cys	Asn	Ile	Ser	Phe	Gly	Gly	Arg	Arg	Met
65				70					75						80
Met	Thr	Cys	Gln	Ile	Ser	Asp	Gly	Ser	Gly	Ile	Leu	Thr	Met	Arg	Phe
			85					90					95		
Phe	Asn	Phe	Ser	Ala	Ala	Met	Lys	Asn	Ser	Leu	Ala	Ala	Gly	Arg	Arg
			100				105						110		
Val	Leu	Ala	Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Lys	Tyr	Gly	Ala	Glu	Met
		115					120					125			
Ile	His	Pro	Glu	Tyr	Arg	Val	Gln	Gly	Asp	Leu	Ser	Thr	Pro	Glu	Leu
	130					135					140				
Gln	Glu	Thr	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Val	Lys	Gln
145					150					155					160
Ala	Thr	Leu	Arg	Lys	Leu	Thr	Asp	Gln	Ala	Leu	Asp	Leu	Leu	Asp	Thr
				165				170						175	
Cys	Ala	Ile	Glu	Glu	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Gln	Gly	Met	Met
		180					185						190		
Thr	Leu	Pro	Glu	Ala	Leu	Arg	Thr	Leu	His	Arg	Pro	Pro	Pro	Thr	Leu
		195					200					205			
Gln	Leu	Ser	Asp	Leu	Glu	Thr	Gly	Gln	His	Pro	Ala	Gln	Arg	Arg	Leu
	210					215					220				

675
Arg Tyr Ser Asn Ala
690

680

685

<210> 394
<211> 428
<212> PRT
<213> Escherichia coli

<400> 394

Met	Lys	Thr	Ser	Leu	Phe	Lys	Ser	Leu	Tyr	Phe	Gln	Val	Leu	Thr	Ala
1				5					10					15	
Ile	Ala	Ile	Gly	Ile	Leu	Leu	Gly	His	Phe	Tyr	Pro	Glu	Ile	Gly	Glu
			20					25					30		
Gln	Met	Lys	Pro	Leu	Gly	Asp	Gly	Phe	Val	Lys	Leu	Ile	Lys	Met	Ile
		35					40					45			
Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met
	50					55					60				
Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr
65				70					75					80	
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val
			85						90					95	
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu
			100					105					110		
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly
		115					120					125			
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala
	130					135					140				
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe
145				150					155					160	
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn
			165					170					175		
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile
		180					185						190		
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile
	195					200					205				
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile
	210				215					220					
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser
225				230					235					240	
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile
			245					250					255		
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu	Gly	Thr	Ser	Ser	Ser	Glu	Ser	Ala
		260					265						270		
Leu	Pro	Arg	Met	Leu	Asp	Lys	Met	Glu	Lys	Leu	Gly	Cys	Arg	Lys	Ser
	275					280					285				
Val	Val	Gly	Leu	Val	Ile	Pro	Thr	Gly	Tyr	Ser	Phe	Asn	Leu	Asp	Gly
	290				295						300				
Thr	Ser	Ile	Tyr	Leu	Thr	Met	Ala	Ala	Val	Phe	Ile	Ala	Gln	Ala	Thr
305				310					315					320	
Asn	Ser	Gln	Met	Asp	Ile	Val	His	Gln	Ile	Thr	Leu	Leu	Ile	Val	Leu
			325					330					335		
Leu	Leu	Ser	Ser	Lys	Gly	Ala	Ala	Gly	Val	Thr	Gly	Ser	Gly	Phe	Ile
		340				345					350				
Val	Leu	Ala	Ala	Thr	Leu	Ser	Ala	Val	Gly	His	Leu	Pro	Val	Ala	Gly
	355					360					365				

BBE"334260

Leu Ala Leu Ile Leu Gly Ile Asp Arg Phe Met Ser Glu Ala Arg Ala
 370 375 380
 Leu Thr Asn Leu Val Gly Asn Gly Val Ala Thr Ile Val Val Ala Lys
 385 390 395 400
 Trp Val Lys Glu Leu Asp His Lys Lys Leu Asp Asp Val Leu Asn Asn
 405 410 415
 Arg Ala Pro Asp Gly Lys Thr His Glu Leu Ser Ser
 420 425

<210> 395
 <211> 396
 <212> PRT
 <213> Escherichia coli

<400> 395
 Met Thr Thr Arg Gln His Ser Ser Phe Ala Ile Val Phe Ile Leu Gly
 1 5 10 15
 Leu Leu Ala Met Leu Met Pro Leu Ser Ile Asp Met Tyr Leu Pro Ala
 20 25 30
 Leu Pro Val Ile Ser Ala Gln Phe Gly Val Pro Ala Gly Ser Thr Gln
 35 40 45
 Met Thr Leu Ser Thr Tyr Ile Leu Gly Phe Ala Leu Gly Gln Leu Ile
 50 55 60
 Tyr Gly Pro Met Ala Asp Ser Phe Gly Arg Lys Pro Val Val Leu Gly
 65 70 75 80
 Gly Thr Leu Val Phe Ala Ala Ala Val Ala Cys Ala Leu Ala Asn
 85 90 95
 Thr Ile Asp Gln Leu Ile Val Met Arg Phe Phe His Gly Leu Ala Ala
 100 105 110
 Ala Ala Ala Ser Val Val Ile Asn Ala Leu Met Arg Asp Ile Tyr Pro
 115 120 125
 Lys Glu Glu Phe Ser Arg Met Met Ser Phe Val Met Leu Val Thr Thr
 130 135 140
 Ile Ala Pro Leu Met Ala Pro Ile Val Gly Gly Trp Val Leu Val Trp
 145 150 155 160
 Leu Ser Trp His Tyr Ile Phe Trp Ile Leu Ala Leu Ala Ala Ile Leu
 165 170 175
 Ala Ser Ala Met Ile Phe Phe Leu Ile Lys Glu Thr Leu Pro Pro Glu
 180 185 190
 Arg Arg Gln Pro Phe His Ile Arg Thr Thr Ile Gly Asn Phe Ala Ala
 195 200 205
 Leu Phe Arg His Lys Arg Val Leu Ser Tyr Met Leu Ala Ser Gly Phe
 210 215 220
 Ser Phe Ala Gly Met Phe Ser Phe Leu Ser Ala Gly Pro Phe Val Tyr
 225 230 235 240
 Ile Glu Ile Asn His Val Ala Pro Glu Asn Phe Gly Tyr Tyr Phe Ala
 245 250 255
 Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
 260 265 270
 Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
 275 280 285
 Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
 290 295 300
 Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
 305 310 315 320
 Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro

<211> 238
 <212> PRT
 <213> Escherichia coli

<400> 398

Met	Gly	Arg	Lys	Trp	Ala	Asn	Ile	Val	Ala	Lys	Lys	Thr	Ala	Lys	Asp
1				5					10					15	
Gly	Ala	Thr	Ser	Lys	Ile	Tyr	Ala	Lys	Phe	Gly	Val	Glu	Ile	Tyr	Ala
			20					25					30		
Ala	Ala	Lys	Gln	Gly	Glu	Pro	Asp	Pro	Glu	Leu	Asn	Thr	Ser	Leu	Lys
		35					40					45			
Phe	Val	Ile	Glu	Arg	Ala	Lys	Gln	Ala	Gln	Val	Pro	Lys	His	Val	Ile
	50					55					60				
Asp	Lys	Ala	Ile	Asp	Lys	Ala	Lys	Gly	Gly	Gly	Asp	Glu	Thr	Phe	Val
65					70					75					80
Gln	Gly	Arg	Tyr	Glu	Gly	Phe	Gly	Pro	Asn	Gly	Ser	Met	Ile	Ile	Ala
			85					90					95		
Glu	Thr	Leu	Thr	Ser	Asn	Val	Asn	Arg	Thr	Ile	Ala	Asn	Val	Arg	Thr
			100					105					110		
Ile	Phe	Asn	Lys	Lys	Gly	Gly	Asn	Ile	Gly	Ala	Ala	Gly	Ser	Val	Ser
		115					120					125			
Tyr	Met	Phe	Asp	Asn	Thr	Gly	Val	Ile	Val	Phe	Lys	Gly	Thr	Asp	Pro
	130					135					140				
Asp	His	Ile	Phe	Glu	Ile	Leu	Leu	Glu	Ala	Glu	Val	Asp	Val	Arg	Asp
145					150					155					160
Val	Thr	Glu	Glu	Glu	Gly	Asn	Ile	Val	Ile	Tyr	Thr	Glu	Pro	Thr	Asp
			165					170					175		
Leu	His	Lys	Gly	Ile	Ala	Ala	Leu	Lys	Ala	Ala	Gly	Ile	Thr	Glu	Phe
			180					185					190		
Ser	Thr	Thr	Glu	Leu	Glu	Met	Ile	Ala	Gln	Ser	Glu	Val	Glu	Leu	Ser
		195				200						205			
Pro	Glu	Asp	Leu	Glu	Ile	Phe	Glu	Gly	Leu	Val	Asp	Ala	Leu	Glu	Asp
	210					215					220				
Asp	Asp	Asp	Val	Gln	Lys	Val	Tyr	His	Asn	Val	Ala	Asn	Leu		
225					230					235					

<210> 399
 <211> 261
 <212> PRT
 <213> Escherichia coli

<400> 399

Met	Val	Leu	Met	Ser	Glu	Thr	Lys	Asn	Glu	Leu	Glu	Asp	Leu	Leu	Glu
1				5					10					15	
Lys	Ala	Ala	Thr	Glu	Pro	Ala	His	Arg	Pro	Ala	Phe	Phe	Arg	Thr	Leu
			20					25					30		
Leu	Glu	Ser	Thr	Val	Trp	Val	Pro	Gly	Thr	Ala	Ala	Gln	Gly	Glu	Ala
		35					40					45			
Val	Val	Glu	Asp	Ser	Ala	Leu	Asp	Leu	Gln	His	Trp	Glu	Lys	Glu	Asp
	50					55					60				
Gly	Thr	Ser	Val	Ile	Pro	Phe	Phe	Thr	Ser	Leu	Glu	Ala	Leu	Gln	Gln
65					70					75					80
Ala	Val	Glu	Asp	Glu	Gln	Ala	Phe	Val	Val	Met	Pro	Val	Arg	Thr	Leu
			85					90					95		
Phe	Glu	Met	Thr	Leu	Gly	Glu	Thr	Leu	Phe	Leu	Asn	Ala	Lys	Leu	Pro
			100					105					110		

Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu
 115 120 125
 Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser
 130 135 140
 Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser
 145 150 155 160
 Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile
 165 170 175
 Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly
 180 185 190
 Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser
 195 200 205
 Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln
 210 215 220
 Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile
 225 230 235 240
 Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys
 245 250 255
 Gln Asn Arg Ile Ile
 260

<210> 400
 <211> 421
 <212> PRT
 <213> Escherichia coli

<400> 400
 Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys
 1 5 10 15
 Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile
 20 25 30
 Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala
 35 40 45
 Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile
 50 55 60
 Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu
 65 70 75 80
 Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr
 85 90 95
 Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met
 100 105 110
 Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser
 115 120 125
 Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile
 130 135 140
 Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe
 145 150 155 160
 Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu
 165 170 175
 Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys
 180 185 190
 Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys
 195 200 205
 Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile
 210 215 220
 Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe

Gly	Asp	Ile	Lys	Pro	Leu	Gln	Gln	Ala	Gly	Val	Tyr	Leu	Ala	Val	Met
			260					265					270		
Asn	Gln	Ala	Gly	Arg	Tyr	Asp	Tyr	Ser	Asn	Pro	Ala	Thr	Leu	Phe	Thr
		275				280						285			
Leu	Ser	Asp	Ile	Gly	Val	Ser	Ala	His	Arg	Tyr	His	Asn	Arg	Leu	Asp
		290				295					300				
Ile	Phe	Thr	Gln	Ser	Leu	Glu	Asn	Gly	Ala	Ala	Gln	Gln	Gly	Ile	Glu
305					310					315					320
Val	Ser	Leu	Leu	Asn	Glu	Lys	Gly	Gln	Thr	Leu	Thr	Gln	Ala	Thr	Ser
				325					330					335	
Asp	Ala	Gln	Gly	His	Val	Gln	Leu	Glu	Asn	Asp	Lys	Asn	Ala	Ala	Leu
			340					345					350		
Leu	Leu	Ala	Arg	Lys	Asp	Gly	Gln	Thr	Thr	Leu	Leu	Asp	Leu	Lys	Leu
		355				360						365			
Pro	Ala	Leu	Asp	Leu	Ala	Glu	Phe	Asn	Ile	Ala	Gly	Ala	Pro	Gly	Tyr
		370				375					380				
Ser	Lys	Gln	Phe	Phe	Met	Phe	Gly	Pro	Arg	Asp	Leu	Tyr	Arg	Pro	Gly
385					390					395					400
Glu	Thr	Val	Ile	Leu	Asn	Gly	Leu	Leu	Arg	Asp	Ala	Asp	Gly	Lys	Ala
				405					410					415	
Leu	Pro	Asn	Gln	Pro	Ile	Lys	Leu	Asp	Val	Ile	Lys	Pro	Asp	Gly	Gln
			420					425					430		
Val	Leu	Arg	Ser	Val	Val	Ser	Gln	Pro	Glu	Asn	Gly	Leu	Tyr	His	Phe
		435					440					445			
Thr	Trp	Pro	Leu	Asp	Ser	Asn	Ala	Ala	Thr	Gly	Met	Trp	His	Ile	Arg
		450				455					460				
Ala	Asn	Thr	Gly	Asp	Asn	Gln	Tyr	Arg	Met	Trp	Asp	Phe	His	Val	Glu
465					470					475					480
Asp	Phe	Met	Pro	Glu	Arg	Met	Ala	Leu	Asn	Leu	Thr	Gly	Glu	Lys	Thr
				485					490					495	
Pro	Leu	Thr	Pro	Lys	Asp	Glu	Val	Lys	Phe	Ser	Val	Val	Gly	Tyr	Tyr
			500					505					510		
Leu	Tyr	Gly	Ala	Pro	Ala	Asn	Gly	Asn	Thr	Leu	Gln	Gly	Gln	Leu	Phe
		515				520						525			
Leu	Arg	Pro	Leu	Arg	Glu	Ala	Val	Ser	Ala	Leu	Pro	Gly	Phe	Glu	Phe
		530				535					540				
Gly	Asp	Ile	Ala	Ala	Glu	Asn	Leu	Ser	Arg	Thr	Leu	Asp	Glu	Val	Gln
545					550					555					560
Leu	Thr	Leu	Asp	Asp	Lys	Gly	Arg	Gly	Glu	Val	Ser	Thr	Glu	Ser	Gln
				565					570					575	
Trp	Lys	Glu	Thr	His	Ser	Pro	Leu	Gln	Val	Ile	Phe	Gln	Gly	Ser	Leu
			580					585					590		
Leu	Glu	Ser	Gly	Gly	Arg	Pro	Val	Thr	Arg	Arg	Ala	Glu	Gln	Ala	Ile
		595					600					605			
Trp	Pro	Ala	Asp	Ala	Leu	Pro	Gly	Ile	Arg	Pro	Gln	Phe	Ala	Ser	Lys
		610				615					620				
Ser	Val	Tyr	Asp	Tyr	Arg	Thr	Asp	Ser	Thr	Val	Lys	Gln	Pro	Ile	Val
625					630					635					640
Asp	Glu	Gly	Ser	Asn	Ala	Ala	Phe	Asp	Ile	Val	Tyr	Ser	Asp	Ala	Gln
				645					650					655	
Gly	Val	Lys	Lys	Ala	Val	Ser	Gly	Leu	Gln	Val	Arg	Leu	Ile	Arg	Glu
				660				665					670		
Arg	Arg	Asp	Tyr	Tyr	Trp	Asn	Trp	Ser	Glu	Asp	Glu	Gly	Trp	Gln	Ser
		675				680						685			
Gln	Phe	Asp	Gln	Lys	Asp	Leu	Ile	Glu	Asn	Glu	Gln	Thr	Leu	Asp	Leu
		690				695				700					
Lys	Ala	Asp	Glu	Thr	Gly	Lys	Val	Ser	Phe	Pro	Val	Glu	Trp	Gly	Ala

1620 1625 1630
 Ser Met Tyr Val Pro Gln Trp Arg Ala Thr Gly Ala Ala Glu Asp Leu
 1635 1640 1645
 Leu Ile Val Arg Pro
 1650

<210> 403
 <211> 264
 <212> PRT
 <213> Escherichia coli

<400> 403
 Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly
 1 5 10 15
 Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg
 20 25 30
 His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala
 35 40 45
 Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu
 50 55 60
 Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu
 65 70 75 80
 Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln
 85 90 95
 Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe
 100 105 110
 Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln
 115 120 125
 Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu
 130 135 140
 Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly
 145 150 155 160
 Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu
 165 170 175
 Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu
 180 185 190
 Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn
 195 200 205
 Asp Ile Thr Leu Pro Asn Thr Phe Ser Gln Ser Leu Tyr Asp Val Leu
 210 215 220
 Met His Gln Arg Asn Leu Ala Trp Arg Asp Lys Leu Arg Ala Met Pro
 225 230 235 240
 Pro Gly Arg Tyr Val Val Ala Val Gly Ala Leu His Leu Tyr Gly Glu
 245 250 255
 Gly Asn Leu Pro Gln Met Leu Arg
 260

<210> 404
 <211> 322
 <212> PRT
 <213> Escherichia coli

<400> 404
 Met Asp Asn Phe Leu Ala Leu Thr Leu Thr Gly Lys Lys Pro Val Ile
 1 5 10 15

<210> 409
 <211> 1048
 <212> PRT
 <213> Escherichia coli

<400> 409

Met	Lys	Ile	Leu	Ser	Leu	Arg	Leu	Lys	Asn	Leu	Asn	Ser	Leu	Lys	Gly
1				5					10					15	
Glu	Trp	Lys	Ile	Asp	Phe	Thr	Arg	Glu	Pro	Phe	Ala	Ser	Asn	Gly	Leu
			20					25					30		
Phe	Ala	Ile	Thr	Gly	Pro	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Asp
		35					40					45			
Ala	Ile	Cys	Leu	Ala	Leu	Tyr	His	Glu	Thr	Pro	Arg	Leu	Ser	Asn	Val
	50					55					60				
Ser	Gln	Ser	Gln	Asn	Asp	Leu	Met	Thr	Arg	Asp	Thr	Ala	Glu	Cys	Leu
65					70					75					80
Ala	Glu	Val	Glu	Phe	Glu	Val	Lys	Gly	Glu	Ala	Tyr	Arg	Ala	Phe	Trp
				85					90					95	
Ser	Gln	Asn	Arg	Ala	Arg	Asn	Gln	Pro	Asp	Gly	Asn	Leu	Gln	Val	Pro
			100					105					110		
Arg	Val	Glu	Leu	Ala	Arg	Cys	Ala	Asp	Gly	Lys	Ile	Leu	Ala	Asp	Lys
		115					120						125		
Val	Lys	Asp	Lys	Leu	Glu	Leu	Thr	Ala	Thr	Leu	Thr	Gly	Leu	Asp	Tyr
	130					135					140				
Gly	Arg	Phe	Thr	Arg	Ser	Met	Leu	Leu	Ser	Gln	Gly	Gln	Phe	Ala	Ala
145					150					155					160
Phe	Leu	Asn	Ala	Lys	Pro	Lys	Glu	Arg	Ala	Glu	Leu	Leu	Glu	Glu	Leu
				165					170					175	
Thr	Gly	Thr	Glu	Ile	Tyr	Gly	Gln	Ile	Ser	Ala	Met	Val	Phe	Glu	Gln
			180					185					190		
His	Lys	Ser	Ala	Arg	Thr	Glu	Leu	Glu	Lys	Leu	Gln	Ala	Gln	Ala	Ser
		195					200					205			
Gly	Val	Thr	Leu	Leu	Thr	Pro	Glu	Gln	Val	Gln	Ser	Leu	Thr	Ala	Ser
	210					215					220				
Leu	Gln	Val	Leu	Thr	Asp	Glu	Glu	Lys	Gln	Leu	Ile	Thr	Ala	Gln	Gln
225					230					235					240
Gln	Glu	Gln	Gln	Ser	Leu	Asn	Trp	Leu	Thr	Arg	Gln	Asp	Glu	Leu	Gln
				245						250				255	
Gln	Glu	Ala	Ser	Arg	Arg	Gln	Gln	Ala	Leu	Gln	Gln	Ala	Leu	Ala	Glu
		260						265					270		
Glu	Glu	Lys	Ala	Gln	Pro	Gln	Leu	Ala	Ala	Leu	Ser	Leu	Ala	Gln	Pro
		275					280					285			
Ala	Arg	Asn	Leu	Arg	Pro	His	Trp	Glu	Arg	Ile	Ala	Glu	His	Ser	Ala
	290					295					300				
Ala	Leu	Ala	His	Ile	Arg	Gln	Gln	Ile	Glu	Glu	Val	Asn	Thr	Arg	Leu
305					310					315					320
Gln	Ser	Thr	Met	Ala	Leu	Arg	Ala	Ser	Ile	Arg	His	His	Ala	Ala	Lys
			325						330					335	
Gln	Ser	Ala	Glu	Leu	Gln	Gln	Gln	Gln	Gln	Ser	Leu	Asn	Thr	Trp	Leu
		340						345					350		
Gln	Glu	His	Asp	Arg	Phe	Arg	Gln	Trp	Asn	Asn	Glu	Pro	Ala	Gly	Trp
		355					360					365			
Arg	Ala	Gln	Phe	Ser	Gln	Gln	Thr	Ser	Asp	Arg	Glu	His	Leu	Arg	Gln
	370					375						380			

Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe
 305 310 315 320
 Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala
 325 330 335
 Ala Lys Val Gln Leu Val Phe
 340

<210> 413
 <211> 548
 <212> PRT
 <213> Escherichia coli

<400> 413
 Met Asp Ser Gln Arg Asn Leu Leu Val Ile Ala Leu Leu Phe Val Ser
 1 5 10 15
 Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln
 20 25 30
 Ala Gln Gln Thr Thr Gln Thr Thr Thr Thr Ala Ala Gly Ser Ala Ala
 35 40 45
 Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys
 50 55 60
 Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu
 65 70 75 80
 Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro
 85 90 95
 Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser
 100 105 110
 Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg
 115 120 125
 Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln
 130 135 140
 Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr
 145 150 155 160
 Phe Thr Lys Thr Phe Val Leu Lys Arg Gly Asp Tyr Ala Val Asn Val
 165 170 175
 Asn Tyr Asn Val Gln Asn Ala Gly Glu Lys Pro Leu Glu Ile Ser Ser
 180 185 190
 Phe Gly Gln Leu Lys Gln Ser Ile Thr Leu Pro Pro His Leu Asp Thr
 195 200 205
 Gly Ser Ser Asn Phe Ala Leu His Thr Phe Arg Gly Ala Ala Tyr Ser
 210 215 220
 Thr Pro Asp Glu Lys Tyr Glu Lys Tyr Lys Phe Asp Thr Ile Ala Asp
 225 230 235 240
 Asn Glu Asn Leu Asn Ile Ser Ser Lys Gly Gly Trp Val Ala Met Leu
 245 250 255
 Gln Gln Tyr Phe Ala Thr Ala Trp Ile Pro His Asn Asp Gly Thr Asn
 260 265 270
 Asn Phe Tyr Thr Ala Asn Leu Gly Asn Gly Ile Ala Ala Ile Gly Tyr
 275 280 285
 Lys Ser Gln Pro Val Leu Val Gln Pro Gly Gln Thr Gly Ala Met Asn
 290 295 300
 Ser Thr Leu Trp Val Gly Pro Glu Ile Gln Asp Lys Met Ala Ala Val
 305 310 315 320
 Ala Pro His Leu Asp Leu Thr Val Asp Tyr Gly Trp Leu Trp Phe Ile
 325 330 335
 Ser Gln Pro Leu Phe Lys Leu Leu Lys Trp Ile His Ser Phe Val Gly

<213> Escherichia coli

<400> 417

Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
1 5 10 15
Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
20 25 30
Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
35 40 45
Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
50 55 60
Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
65 70 75 80
Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln
85 90 95
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly
100 105 110
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp
115 120 125
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp
130 135 140
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser
145 150 155 160
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys
165 170 175
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg
180 185 190
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu
195 200 205
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile
210 215 220
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys
225 230 235 240
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val
245 250 255
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn
260 265 270
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu
275 280 285
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn
290 295 300

<210> 418

<211> 328

<212> PRT

<213> Escherichia coli

<400> 418

Met Asn Asn Ser Ala Phe Thr Phe Gln Thr Leu His Pro Asp Thr Ile
1 5 10 15
Met Asp Ala Leu Phe Glu His Gly Ile Arg Val Asp Ser Gly Leu Thr
20 25 30
Pro Leu Asn Ser Tyr Glu Asn Arg Val Tyr Gln Phe Gln Asp Glu Asp
35 40 45
Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala
50 55 60

115	120	125
Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala		
130	135	140
Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala		
145	150	155
Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly		
165	170	175
Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val		
180	185	190
Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys		
195	200	205

<210> 420
 <211> 112
 <212> PRT
 <213> Escherichia coli

<400> 420
Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
1 5 10 15
Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
20 25 30
Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
35 40 45
Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
50 55 60
Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
65 70 75 80
Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
85 90 95
Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
100 105 110

<210> 421
 <211> 346
 <212> PRT
 <213> Escherichia coli

<400> 421
Met Lys Ser Val Val Asn Asp Thr Asp Gly Ile Val Arg Val Ala Glu
1 5 10 15
Ser Val Ile Pro Glu Ile Lys His Gln Asp Glu Val Arg Val Lys Ile
20 25 30
Ala Ser Ser Gly Leu Cys Gly Ser Asp Leu Pro Arg Ile Phe Lys Asn
35 40 45
Gly Ala His Tyr Tyr Pro Ile Thr Leu Gly His Glu Phe Ser Gly Tyr
50 55 60
Ile Asp Ala Val Gly Ser Gly Val Asp Asp Leu His Pro Gly Asp Ala
65 70 75 80
Val Ala Cys Val Pro Leu Leu Pro Cys Phe Thr Cys Pro Glu Cys Leu
85 90 95
Lys Gly Phe Tyr Ser Gln Cys Ala Lys Tyr Asp Phe Ile Gly Ser Arg
100 105 110
Arg Asp Gly Gly Phe Ala Glu Tyr Ile Val Val Lys Arg Lys Asn Val
115 120 125

Phe Ala Leu Pro Thr Asp Met Pro Ile Glu Asp Gly Ala Phe Ile Glu
 130 135 140
 Pro Ile Thr Val Gly Leu His Ala Phe His Leu Ala Gln Gly Cys Glu
 145 150 155 160
 Asn Lys Asn Val Ile Ile Ile Gly Ala Gly Thr Ile Gly Leu Leu Ala
 165 170 175
 Ile Gln Cys Ala Val Ala Leu Gly Ala Lys Ser Val Thr Ala Ile Asp
 180 185 190
 Ile Ser Ser Glu Lys Leu Ala Leu Ala Lys Ser Phe Gly Ala Met Gln
 195 200 205
 Thr Phe Asn Ser Ser Glu Met Ser Ala Pro Gln Met Gln Ser Val Leu
 210 215 220
 Arg Glu Leu Arg Phe Asn Gln Leu Ile Leu Glu Thr Ala Gly Val Pro
 225 230 235 240
 Gln Thr Val Glu Leu Ala Val Glu Ile Ala Gly Pro His Ala Gln Leu
 245 250 255
 Ala Leu Val Gly Thr Leu His Gln Asp Leu His Leu Thr Ser Ala Thr
 260 265 270
 Phe Gly Lys Ile Leu Arg Lys Glu Leu Thr Val Ile Gly Ser Trp Met
 275 280 285
 Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
 290 295 300
 Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
 305 310 315 320
 Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
 325 330 335
 Ala Met Pro Gly Lys Val Leu Leu Ile Pro
 340 345

<210> 422
 <211> 451
 <212> PRT
 <213> Escherichia coli

<400> 422
 Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
 1 5 10 15
 Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
 20 25 30
 Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
 35 40 45
 Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
 50 55 60
 Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
 65 70 75 80
 Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
 85 90 95
 Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
 100 105 110
 Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His
 115 120 125
 Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met
 130 135 140
 Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu
 145 150 155 160
 Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly

<210> 424
 <211> 150
 <212> PRT
 <213> Escherichia coli

<400> 424
 Met Thr Asn Leu Phe Val Arg Ser Gly Ile Ser Phe Val Asp Arg Ser
 1 5 10 15
 Glu Val Leu Thr His Ile Gly Asn Glu Met Leu Ala Lys Gly Val Val
 20 25 30
 His Asp Thr Trp Pro Gln Ala Leu Ile Ala Arg Glu Ala Glu Phe Pro
 35 40 45
 Thr Gly Ile Met Leu Glu Gln His Ala Ile Ala Ile Pro His Cys Glu
 50 55 60
 Ala Ile His Ala Lys Ser Ser Ala Ile Tyr Leu Leu Arg Pro Thr Asn
 65 70 75 80
 Lys Val His Phe Gln Gln Ala Asp Asp Asp Asn Asp Val Ala Val Ser
 85 90 95
 Leu Val Ile Ala Leu Ile Val Glu Asn Pro Gln Gln Gln Leu Lys Leu
 100 105 110
 Leu Arg Cys Leu Phe Gly Lys Leu Gln Gln Pro Asp Ile Val Glu Thr
 115 120 125
 Leu Ile Thr Leu Pro Glu Thr Gln Leu Lys Glu Tyr Phe Thr Lys Tyr
 130 135 140
 Val Leu Asp Ser Asp Glu
 145 150

<210> 425
 <211> 420
 <212> PRT
 <213> Escherichia coli

<400> 425
 Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
 1 5 10 15
 Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
 20 25 30
 Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
 35 40 45
 Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
 50 55 60
 Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
 65 70 75 80
 Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
 85 90 95
 Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
 100 105 110
 Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
 115 120 125
 Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
 130 135 140
 Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
 145 150 155 160
 Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly

Phe	Asp	Val	Ser	Val	Glu	Ala	Glu	Leu	Gly	Gln	Leu	Gly	Gly	Gln	Glu
130						135					140				
Asp	Asp	Val	Gln	Val	Asn	Glu	Ala	Asp	Ala	Leu	Tyr	Thr	Asn	Pro	Ala
145					150					155					160
Gln	Ala	Arg	Glu	Phe	Ala	Glu	Ala	Thr	Gly	Ile	Asp	Ser	Leu	Ala	Val
				165					170					175	
Ala	Ile	Gly	Thr	Ala	His	Gly	Met	Tyr	Ala	Ser	Ala	Pro	Ala	Leu	Asp
			180					185					190		
Phe	Ser	Arg	Leu	Glu	Asn	Ile	Arg	Gln	Trp	Val	Asn	Leu	Pro	Leu	Val
	195						200					205			
Leu	His	Gly	Ala	Ser	Gly	Leu	Ser	Thr	Lys	Asp	Ile	Gln	Gln	Thr	Ile
210						215					220				
Lys	Leu	Gly	Ile	Cys	Lys	Ile	Asn	Val	Ala	Thr	Glu	Leu	Lys	Asn	Ala
225					230					235					240
Phe	Ser	Gln	Ala	Leu	Lys	Asn	Tyr	Leu	Thr	Glu	His	Pro	Glu	Ala	Thr
				245					250					255	
Asp	Pro	Arg	Asp	Tyr	Leu	Gln	Ser	Ala	Lys	Ser	Ala	Met	Arg	Asp	Val
			260					265					270		
Val	Ser	Lys	Val	Ile	Ala	Asp	Cys	Gly	Cys	Glu	Gly	Arg	Ala		
	275						280					285			

<210> 427
 <211> 157
 <212> PRT
 <213> Escherichia coli

<400> 427

Met	Ser	Gln	Asn	Asp	Ile	Ile	Ile	Arg	Thr	His	Tyr	Lys	Ser	Pro	His
1				5					10					15	
Arg	Leu	His	Ile	Asp	Ser	Asp	Ile	Pro	Thr	Pro	Ser	Ser	Glu	Pro	Ile
			20					25					30		
Asn	Gln	Phe	Ala	Arg	Gln	Leu	Ile	Thr	Leu	Leu	Asp	Thr	Ser	Asp	Leu
		35				40						45			
Ser	Ser	Met	Leu	Ser	Tyr	Cys	Val	Thr	Gln	Glu	Phe	Thr	Ala	Asn	Cys
	50					55					60				
Arg	Lys	Ile	Ser	Gln	Asn	Cys	Tyr	Ser	Thr	Ala	Leu	Phe	Thr	Ile	Asn
65					70					75					80
Phe	Ala	Thr	Ser	Pro	Ile	His	Thr	Glu	Asn	Ile	Leu	Ile	Thr	Leu	His
			85					90						95	
Tyr	Lys	Lys	Glu	Ile	Ile	Ser	Leu	Leu	Glu	Thr	Thr	Pro	Ile	Lys	
		100						105					110		
Ala	Asn	His	Leu	Arg	Ser	Ile	Leu	Asp	Tyr	Ile	Glu	Gln	Glu	Gln	Leu
	115						120					125			
Thr	Ala	Glu	Asp	Arg	Asn	His	Cys	Met	Lys	Leu	Ser	Lys	Lys	Ile	His
	130					135					140				
Arg	Glu	Lys	Asn	Tyr	Thr	Pro	Asn	Ser	Lys	Ser	Gln	Trp			
145					150						155				

<210> 428
 <211> 471
 <212> PRT
 <213> Escherichia coli

<400> 428
 Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln

1	5	10	15
Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile			
	20	25	30
Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val			
	35	40	45
Arg Asp Ala Glu Phe Arg Ala Leu Leu Arg His Pro Pro Ala Gly Ser			
	50	55	60
Arg Val Ile Ala Ser Lys Asp Phe Gly Phe Ala Leu Asp Ile Phe Phe			
65	70	75	80
Cys Arg Met Met Ala Asn Asn Val Ser His Met Ser Ala Ile Leu Tyr			
	85	90	95
Ile Asp Asn His Thr Leu Ser Val Arg Leu Arg Ile Lys Gln Ser Val			
	100	105	110
Tyr Gly Gln Leu Asn Tyr Val Val Ser Val Tyr Asp Pro Asn Asp Thr			
	115	120	125
Asn Val Ala Val Arg Asp Thr His Arg Thr Ala Arg Gly Phe Leu Ser			
	130	135	140
Leu Asp Lys Phe Ile Ser Ser Gly Pro Asp Ala Gln Thr Trp Ala Asp			
145	150	155	160
Arg Tyr Val Arg Asn Cys Ala Ile Ala Ile Leu Pro Leu Leu Pro Val			
	165	170	175
Gly Val Pro Gly Ala Ile Phe Ala Gly Ile Ala Ser Arg Met Pro Phe			
	180	185	190
Ala Pro Ile His Pro Ser Ala Met Leu Leu Ile Met Ala Thr Gly Gln			
	195	200	205
Ser Gln Gln Leu Ile Thr Leu Phe Lys Gln Leu Pro Ile Leu Pro Glu			
	210	215	220
Lys Glu Ile Ile Glu Ile Thr Ala Gln Asn Ser Val Gly Thr Pro			
225	230	235	240
Ala Leu Phe Leu Ala Met Met Asn Gly His Thr Asp Asn Val Lys Ile			
	245	250	255
Phe Met Gln Glu Ile Gln Ser Leu Val Asp Asn His Ile Ile His Glu			
	260	265	270
Asp Asn Leu Val Lys Leu Leu Gln Thr Lys Ser Ala Asn Glu Thr Pro			
	275	280	285
Gly Leu Tyr Ile Ser Met Leu Tyr Gly Phe Asp Glu Ile Ile Asp Ile			
	290	295	300
Phe Leu Asn Ala Leu Thr Thr Pro Ile Ala Gln Glu Leu Leu Asn Lys			
305	310	315	320
Lys Leu Val Met Ser Ile Leu Ala Met Lys Ile His Asp Gly Glu Pro			
	325	330	335
Gly Leu Tyr Ala Ala Met Glu Asn Asn His Pro Leu Cys Val Thr Arg			
	340	345	350
Phe Leu Ser Lys Ile Asn Gly Ile Ala Phe Lys Tyr Lys Leu Ser Lys			
	355	360	365
Ala Asn Ile Met Asp Leu Leu Lys Gly Ala Thr Ala Gln Gly Thr Pro			
	370	375	380
Ala Leu Tyr Ile Ala Met Ser Lys Gly Asn Glu Asp Val Val Leu Ser			
385	390	395	400
Tyr Ile Ser Thr Leu Gly Ala Phe Ala Lys Lys His Ser Phe Ser Gln			
	405	410	415
His Gln Leu Phe Thr Leu Leu Ala Ala Lys Asn His Asp Asn Met Ser			
	420	425	430
Ala Val His Ile Ala Ile His His Lys His Tyr Lys Thr Val Glu Thr			
	435	440	445
Tyr Tyr Ala Ala Ile Asn Ala Ile Ser Gln Ser Leu Ser Phe Ser Ala			
	450	455	460

Asp Glu Ile Lys Thr Tyr Leu
465 470

<210> 429
<211> 128
<212> PRT
<213> Escherichia coli

<400> 429
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

<210> 430
<211> 398
<212> PRT
<213> Escherichia coli

<400> 430
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30
Asp Ala Ile Ile Pro Ala Tyr Asn Glu Gly Pro Cys Leu Ala Gln Ser
35 40 45
Leu Asp Asn Leu Leu Arg Asn Pro Tyr Phe Cys Arg Val Ile Cys Val
50 55 60
Asn Asp Gly Ser Thr Asp Asn Thr Glu Ala Val Met Ala Glu Val Lys
65 70 75 80
Arg Lys Trp Gly Asp Arg Phe Val Ala Val Thr Gln Lys Asn Thr Gly
85 90 95
Lys Gly Gly Ala Leu Met Asn Gly Leu Asn Tyr Ala Thr Cys Asp Gln
100 105 110
Val Phe Leu Ser Asp Ala Asp Thr Tyr Val Pro Pro Asp Gln Asp Gly
115 120 125
Met Gly Tyr Met Leu Ala Glu Ile Glu Arg Gly Ala Asp Ala Val Gly
130 135 140
Gly Ile Pro Ser Thr Ala Leu Lys Gly Ala Gly Leu Leu Pro His Ile
145 150 155 160
Arg Ala Thr Val Lys Leu Pro Met Ile Val Met Lys Arg Thr Leu Gln
165 170 175
Gln Leu Leu Gly Gly Ala Pro Phe Ile Ile Ser Gly Ala Cys Gly Met

Pro	Asn	Val	Glu	Val	Thr	Ala	Arg	Gln	Leu	Asp	Phe	Leu	Ala	Arg	Glu
		180						185					190		
Leu	Ser	Ser	His	Pro	Gln	Asn	Leu	Ser	Asp	Gly	Gln	Ile	Arg	Gln	Gly
		195				200						205			
Leu	Ser	Ala	Met	Val	Gln	Leu	Leu	Glu	His	Tyr	Phe	Ser	Glu	Gln	Gly
		210				215					220				
Ala	Gly	Gln	Ala	Arg	Tyr	Arg	Leu	Met	Arg	Arg	Arg	Ala	Ser	Asn	Glu
225					230					235					240
Gln	Arg	Ser	Trp	Arg	Tyr	Leu	Asp	Ile	Ile	Asn	Arg	Met	Ile	Asp	Arg
			245					250						255	
Pro	Gly	Gly	Arg	Ser	Tyr	Arg	Val	Ile	Leu	Leu	Gly	Leu	Phe	Ala	Thr
			260					265					270		
Leu	Leu	Gln	Ala	Lys	Gly	Thr	Leu	Arg	Leu	Asp	Lys	Asp	Ala	Arg	Pro
		275					280					285			
Leu	Leu	Leu	Ile	Glu	Asp	Pro	Glu	Thr	Arg	Leu	His	Pro	Ile	Met	Leu
		290				295					300				
Ser	Val	Ala	Trp	His	Leu	Leu	Asn	Leu	Leu	Pro	Leu	Gln	Arg	Ile	Ala
305					310					315					320
Thr	Thr	Asn	Ser	Gly	Glu	Leu	Leu	Ser	Leu	Thr	Pro	Val	Glu	His	Val
				325					330					335	
Cys	Arg	Leu	Val	Arg	Glu	Ser	Ser	Arg	Val	Ala	Ala	Trp	Arg	Leu	Gly
			340					345					350		
Pro	Ser	Gly	Leu	Ser	Thr	Glu	Asp	Ser	Arg	Arg	Ile	Ser	Phe	His	Ile
		355					360					365			
Arg	Phe	Asn	Arg	Pro	Ser	Ser	Leu	Phe	Ala	Arg	Cys	Trp	Leu	Leu	Val
		370				375					380				
Glu	Gly	Glu	Thr	Glu	Thr	Trp	Val	Ile	Asn	Glu	Leu	Ala	Arg	Gln	Cys
385					390					395					400
Gly	His	His	Phe	Asp	Ala	Glu	Gly	Ile	Lys	Val	Ile	Glu	Phe	Ala	Gln
				405					410					415	
Ser	Gly	Leu	Lys	Pro	Leu	Val	Lys	Phe	Ala	Arg	Arg	Met	Gly	Ile	Glu
			420					425					430		
Trp	His	Val	Leu	Val	Asp	Gly	Asp	Glu	Ala	Gly	Lys	Lys	Tyr	Ala	Ala
			435				440						445		
Thr	Val	Arg	Ser	Leu	Leu	Asn	Asn	Asp	Arg	Glu	Ala	Glu	Arg	Glu	His
						455					460				
Leu	Thr	Ala	Leu	Pro	Ala	Leu	Asp	Met	Glu	His	Phe	Met	Tyr	Arg	Gln
465					470					475					480
Gly	Phe	Ser	Asp	Val	Phe	His	Arg	Met	Ala	Gln	Ile	Pro	Glu	Asn	Val
				485					490					495	
Pro	Met	Asn	Leu	Arg	Lys	Ile	Ile	Ser	Lys	Ala	Ile	His	Arg	Ser	Ser
			500					505					510		
Lys	Pro	Asp	Leu	Ala	Ile	Glu	Val	Ala	Met	Glu	Ala	Gly	Arg	Arg	Gly
			515				520					525			
Val	Asp	Ser	Val	Pro	Thr	Leu	Leu	Lys	Lys	Met	Phe	Ser	Arg	Val	Leu
			530			535					540				
Trp	Leu	Ala	Arg	Gly	Arg	Ala	Asp								
545					550										

<210> 432

<211> 352

<212> PRT

<213> Escherichia coli

<400> 432

Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu

Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser
 50 55 60
 Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu
 65 70 75 80
 Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr
 85 90 95
 Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala
 100 105 110
 Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser
 115 120 125
 Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu
 130 135 140
 Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val
 145 150 155 160
 Ser Leu Glu Thr Arg Met Arg Phe Asn Pro Asn Leu Asp Pro Ala Trp
 165 170 175
 Phe Gly Gly Val Met Ala Ile Ile Asn Asn Ile Thr Met Leu Ala Ile
 180 185 190
 Val Leu Thr Gly Ser Ala Leu Ile Arg Glu Arg Glu His Gly Thr Val
 195 200 205
 Glu His Leu Leu Val Met Pro Ile Thr Pro Phe Glu Ile Met Met Ala
 210 215 220
 Lys Ile Trp Ser Met Gly Leu Val Val Leu Val Val Ser Gly Leu Ser
 225 230 235 240
 Leu Val Leu Met Val Lys Gly Val Leu Gly Val Pro Ile Glu Gly Ser
 245 250 255
 Ile Pro Leu Phe Met Leu Gly Val Ala Leu Ser Leu Phe Ala Thr Thr
 260 265 270
 Ser Ile Gly Ile Phe Met Gly Thr Ile Ala Arg Ser Met Pro Gln Leu
 275 280 285
 Gly Leu Leu Val Ile Leu Val Leu Leu Pro Leu Gln Met Leu Ser Gly
 290 295 300
 Gly Ser Thr Pro Arg Glu Ser Met Pro Gln Met Val Gln Asp Ile Met
 305 310 315 320
 Leu Thr Met Pro Thr Thr His Phe Val Ser Leu Ala Gln Ala Ile Leu
 325 330 335
 Tyr Arg Gly Ala Gly Phe Glu Ile Val Trp Pro Gln Phe Leu Thr Leu
 340 345 350
 Met Ala Ile Gly Gly Ala Phe Phe Thr Ile Ala Leu Leu Arg Phe Arg
 355 360 365
 Lys Thr Ile Gly Thr Met Ala
 370 375

<210> 434
 <211> 894
 <212> PRT
 <213> Escherichia coli

<400> 434
 Met Ser Gln His Tyr Gly Lys Thr Val Ala Leu Asn Asn Ile Thr Leu
 1 5 10 15
 Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val
 20 25 30
 Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu
 35 40 45
 Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His

00011569 1200

Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys
 35 40 45
 Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln
 50 55 60
 Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val
 65 70 75 80
 Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln
 85 90 95
 Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr
 100 105 110
 Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu
 115 120 125
 Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly
 130 135 140
 Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys
 145 150 155 160
 Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr
 165 170 175
 Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr
 180 185 190
 Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu
 195 200 205
 Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
 210 215 220
 Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser
 225 230 235

<210> 437
 <211> 480
 <212> PRT
 <213> Escherichia coli

<400> 437

Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro
 1 5 10 15
 Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala
 20 25 30
 Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys
 35 40 45
 Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His
 50 55 60
 Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr
 65 70 75 80
 Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu
 85 90 95
 Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile
 100 105 110
 Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu
 115 120 125
 Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met
 130 135 140
 Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys
 145 150 155 160
 Gly Ile Asn Lys Leu Gly Gly Gly Leu Ser Ala Glu Ala Leu Thr Glu
 165 170 175
 Lys Asp Lys Ala Asp Ile Lys Thr Ala Ala Leu Ile Gly Val Asp Tyr

His Tyr Gly Val Val Asp Tyr Leu Ile Lys Pro Phe Gln Ala Ser Arg
 100 105 110
 Phe Glu Glu Ala Leu Thr Gly Trp Arg Gln Lys Lys Met Ala Leu Glu
 115 120 125
 Lys His Gln Tyr Tyr Asp Gln Ala Glu Leu Asp Gln Leu Ile His Gly
 130 135 140
 Ser Ser Ser Asn Glu Gln Asp Pro Arg Arg Leu Pro Lys Gly Leu Thr
 145 150 155 160
 Pro Gln Thr Leu Arg Thr Leu Cys Gln Trp Ile Asp Ala His Gln Asp
 165 170 175
 Tyr Glu Phe Ser Thr Asp Glu Leu Ala Asn Glu Val Asn Ile Ser Arg
 180 185 190
 Val Ser Cys Arg Lys Tyr Leu Ile Trp Leu Val Asn Cys His Ile Leu
 195 200 205
 Phe Thr Ser Ile His Tyr Gly Val Thr Gly Arg Pro Val Tyr Arg Tyr
 210 215 220
 Arg Ile Gln Ala Glu His Tyr Ser Leu Leu Lys Gln Tyr Cys Gln
 225 230 235

<210> 439
 <211> 543
 <212> PRT
 <213> Escherichia coli

<400> 439
 Met Arg His Ser Leu Pro Tyr Arg Met Leu Arg Lys Arg Pro Met Lys
 1 5 10 15
 Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val
 20 25 30
 Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr
 35 40 45
 Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala
 50 55 60
 Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser
 65 70 75 80
 Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu
 85 90 95
 Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu
 100 105 110
 Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala
 115 120 125
 Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln
 130 135 140
 Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile
 145 150 155 160
 Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile
 165 170 175
 Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu
 180 185 190
 Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile
 195 200 205
 Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg
 210 215 220
 Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp
 225 230 235 240
 Arg Gly Glu Val Thr Leu Ile Asn Asp Ala Ala Gln Glu Leu Leu Asn

				245					250					255			
Tyr	Arg	Lys	Ser	Gln	Asp	Asp	Glu	Lys	Leu	Ser	Thr	Leu	Ser	His	Ser		
			260					265					270				
Trp	Ser	Gln	Val	Val	Asp	Val	Ser	Glu	Val	Leu	Arg	Asp	Gly	Thr	Pro		
		275					280					285					
Arg	Arg	Asp	Glu	Glu	Ile	Thr	Ile	Lys	Asp	Arg	Leu	Leu	Leu	Ile	Asn		
	290					295					300						
Thr	Val	Pro	Val	Arg	Ser	Asn	Gly	Val	Ile	Ile	Gly	Ala	Ile	Ser	Thr		
305					310					315					320		
Phe	Arg	Asp	Lys	Thr	Glu	Val	Arg	Lys	Leu	Met	Gln	Arg	Leu	Asp	Gly		
			325					330						335			
Leu	Val	Asn	Tyr	Ala	Asp	Ala	Leu	Arg	Glu	Arg	Ser	His	Glu	Phe	Met		
		340					345						350				
Asn	Lys	Leu	His	Val	Ile	Leu	Gly	Leu	Leu	His	Leu	Lys	Ser	Tyr	Lys		
	355					360						365					
Gln	Leu	Glu	Asp	Tyr	Ile	Leu	Lys	Thr	Ala	Asn	Asn	Tyr	Gln	Glu	Glu		
	370					375					380						
Ile	Gly	Ser	Leu	Leu	Gly	Lys	Ile	Lys	Ser	Pro	Val	Ile	Ala	Gly	Phe		
385					390					395					400		
Leu	Ile	Ser	Lys	Ile	Asn	Arg	Ala	Thr	Asp	Leu	Gly	His	Thr	Leu	Ile		
			405					410						415			
Leu	Asn	Ser	Glu	Ser	Gln	Leu	Pro	Asp	Ser	Gly	Ser	Glu	Asp	Gln	Val		
		420					425						430				
Ala	Thr	Leu	Ile	Thr	Thr	Leu	Gly	Asn	Leu	Ile	Glu	Asn	Ala	Leu	Glu		
	435						440					445					
Ala	Leu	Gly	Pro	Glu	Pro	Gly	Gly	Glu	Ile	Ser	Val	Thr	Leu	His	Tyr		
	450					455					460						
Arg	His	Gly	Trp	Leu	His	Cys	Glu	Val	Asn	Asp	Asp	Gly	Pro	Gly	Ile		
465					470					475					480		
Ala	Pro	Asp	Lys	Ile	Asp	His	Ile	Phe	Asp	Lys	Gly	Val	Ser	Thr	Lys		
			485					490						495			
Gly	Ser	Glu	Arg	Gly	Val	Gly	Leu	Ala	Leu	Val	Lys	Gln	Gln	Val	Glu		
			500				505					510					
Asn	Leu	Gly	Gly	Ser	Ile	Ala	Val	Glu	Ser	Glu	Pro	Gly	Ile	Phe	Thr		
	515					520						525					
Gln	Phe	Phe	Val	Gln	Ile	Pro	Trp	Asp	Gly	Glu	Arg	Ser	Asn	Arg			
	530					535					540						

<210> 440
 <211> 328
 <212> PRT
 <213> Escherichia coli

<400> 440
 Met Ser Val Pro Leu Ser Thr Trp Asn Leu Leu Arg Tyr Asn Asn Ser
 1 5 10 15
 Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu
 20 25 30
 Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu
 35 40 45
 Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr
 50 55 60
 Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile
 65 70 75 80
 Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu
 85 90 95

Arg Glu Lys Met Ile Ala Glu Asn Phe Arg Ser Leu Gly Met Ala Leu
 100 105 110
 Val Glu Thr Gly Met Ala Trp Phe Trp Pro Asp Ser Arg Val Arg Lys
 115 120 125
 Trp Phe Asp Val Glu Gly Leu Asp Asn Leu Lys Arg Ala Gln Met Gln
 130 135 140
 Asn Arg Gly Val Met Val Val Gly Val His Phe Met Ser Leu Glu Leu
 145 150 155 160
 Gly Gly Arg Val Met Gly Leu Cys Gln Pro Met Met Ala Thr Tyr Arg
 165 170 175
 Pro His Asn Asn Gln Leu Met Glu Trp Val Gln Thr Arg Gly Arg Met
 180 185 190
 Arg Ser Asn Lys Ala Met Ile Gly Arg Asn Asn Leu Arg Gly Ile Val
 195 200 205
 Gly Ala Leu Lys Lys Gly Glu Ala Val Trp Phe Ala Pro Asp Gln Asp
 210 215 220
 Tyr Gly Arg Lys Gly Ser Ser Phe Ala Pro Phe Phe Ala Val Glu Asn
 225 230 235 240
 Val Ala Thr Thr Asn Gly Thr Tyr Val Leu Ser Arg Leu Ser Gly Ala
 245 250 255
 Ala Met Leu Thr Val Thr Met Val Arg Lys Ala Asp Tyr Ser Gly Tyr
 260 265 270
 Arg Leu Phe Ile Thr Pro Glu Met Glu Gly Tyr Pro Thr Asp Glu Asn
 275 280 285
 Gln Ala Ala Tyr Met Asn Lys Ile Ile Glu Lys Glu Ile Met Arg
 290 295 300
 Ala Pro Glu Gln Tyr Leu Trp Ile His Arg Arg Phe Lys Thr Arg Pro
 305 310 315 320
 Val Gly Glu Ser Ser Leu Tyr Ile
 325

<210> 441
 <211> 87
 <212> PRT
 <213> Escherichia coli

<400> 441
 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 Ala Gln Ile Asn Lys Leu Ala
 85

<210> 442
 <211> 430
 <212> PRT
 <213> Escherichia coli

<210> 443
 <211> 883
 <212> PRT
 <213> Escherichia coli

<400> 443

Met	Asn	Glu	Gln	Tyr	Ser	Ala	Leu	Arg	Ser	Asn	Val	Ser	Met	Leu	Gly
1				5					10					15	
Lys	Val	Leu	Gly	Glu	Thr	Ile	Lys	Asp	Ala	Leu	Gly	Glu	His	Ile	Leu
		20						25					30		
Glu	Arg	Val	Glu	Thr	Ile	Arg	Lys	Leu	Ser	Lys	Ser	Ser	Arg	Ala	Gly
		35					40					45			
Asn	Asp	Ala	Asn	Arg	Gln	Glu	Leu	Leu	Thr	Thr	Leu	Gln	Asn	Leu	Ser
	50					55					60				
Asn	Asp	Glu	Leu	Leu	Pro	Val	Ala	Arg	Ala	Phe	Ser	Gln	Phe	Leu	Asn
65					70					75					80
Leu	Ala	Asn	Thr	Ala	Glu	Gln	Tyr	His	Ser	Ile	Ser	Pro	Lys	Gly	Glu
				85					90					95	
Ala	Ala	Ser	Asn	Pro	Glu	Val	Ile	Ala	Arg	Thr	Leu	Arg	Lys	Leu	Lys
			100					105					110		
Asn	Gln	Pro	Glu	Leu	Ser	Glu	Asp	Thr	Ile	Lys	Lys	Ala	Val	Glu	Ser
		115					120						125		
Leu	Ser	Leu	Glu	Leu	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Ile	Thr	Arg
	130					135					140				
Arg	Thr	Leu	Ile	His	Lys	Met	Val	Glu	Val	Asn	Ala	Cys	Leu	Lys	Gln
145					150					155					160
Leu	Asp	Asn	Lys	Asp	Ile	Ala	Asp	Tyr	Glu	His	Asn	Gln	Leu	Met	Arg
			165						170					175	
Arg	Leu	Arg	Gln	Leu	Ile	Ala	Gln	Ser	Trp	His	Thr	Asp	Glu	Ile	Arg
			180					185					190		
Lys	Leu	Arg	Pro	Ser	Pro	Val	Asp	Glu	Ala	Lys	Trp	Gly	Phe	Ala	Val
		195					200					205			
Val	Glu	Asn	Ser	Leu	Trp	Gln	Gly	Val	Pro	Asn	Tyr	Leu	Arg	Glu	Leu
	210					215					220				
Asn	Glu	Gln	Leu	Glu	Glu	Asn	Leu	Gly	Tyr	Lys	Leu	Pro	Val	Glu	Phe
225					230					235					240
Val	Pro	Val	Arg	Phe	Thr	Ser	Trp	Met	Gly	Gly	Asp	Arg	Asp	Gly	Asn
				245					250					255	
Pro	Asn	Val	Thr	Ala	Asp	Ile	Thr	Arg	His	Val	Leu	Leu	Leu	Ser	Arg
		260						265					270		
Trp	Lys	Ala	Thr	Asp	Leu	Phe	Leu	Lys	Asp	Ile	Gln	Val	Leu	Val	Ser
		275					280					285			
Glu	Leu	Ser	Met	Val	Glu	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Leu	Val	Gly
	290					295					300				
Glu	Glu	Gly	Ala	Ala	Glu	Pro	Tyr	Arg	Tyr	Leu	Met	Lys	Asn	Leu	Arg
305					310					315					320
Ser	Arg	Leu	Met	Ala	Thr	Gln	Ala	Trp	Leu	Glu	Ala	Arg	Leu	Lys	Gly
				325					330					335	
Glu	Glu	Leu	Pro	Lys	Pro	Glu	Gly	Leu	Leu	Thr	Gln	Asn	Glu	Glu	Leu
			340					345					350		
Trp	Glu	Pro	Leu	Tyr	Ala	Cys	Tyr	Gln	Ser	Leu	Gln	Ala	Cys	Gly	Met
		355					360						365		
Gly	Ile	Ile	Ala	Asn	Gly	Asp	Leu	Leu	Asp	Thr	Leu	Arg	Arg	Val	Lys
	370					375					380				
Cys	Phe	Gly	Val	Pro	Leu	Val	Arg	Ile	Asp	Ile	Arg	Gln	Glu	Ser	Thr
385					390					395					400
Arg	His	Thr	Glu	Ala	Leu	Gly	Glu	Leu	Thr	Arg	Tyr	Leu	Gly	Ile	Gly

Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
85 90 95
Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
100 105 110
Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
115 120 125
Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
130 135 140
Glu Arg Leu Gln Asp Leu Ser Leu
145 150

<210> 446
<211> 313
<212> PRT
<213> Escherichia coli

<400> 446
Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val
1 5 10 15
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe
20 25 30
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu
35 40 45
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala
50 55 60
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser
65 70 75 80
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp
85 90 95
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala
100 105 110
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met
115 120 125
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu
130 135 140
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe
145 150 155 160
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro
165 170 175
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro
180 185 190
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val
195 200 205
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
210 215 220
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225 230 235 240
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
260 265 270
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300
Leu Arg Ile Ala Glu Arg Thr Asn Ala

<400> 449

Met	Ala	Asp	Arg	Asn	Leu	Arg	Asp	Leu	Leu	Ala	Pro	Trp	Val	Pro	Asp
1				5					10					15	
Ala	Pro	Ser	Arg	Ala	Leu	Arg	Glu	Met	Thr	Leu	Asp	Ser	Arg	Val	Ala
		20					25					30			
Ala	Ala	Gly	Asp	Leu	Phe	Val	Ala	Val	Val	Gly	His	Gln	Ala	Asp	Gly
		35					40					45			
Arg	Arg	Tyr	Ile	Pro	Gln	Ala	Ile	Ala	Gln	Gly	Val	Ala	Ala	Ile	Ile
		50			55						60				
Ala	Glu	Ala	Lys	Asp	Glu	Ala	Thr	Asp	Gly	Glu	Ile	Arg	Glu	Met	His
65					70					75					80
Gly	Val	Pro	Val	Ile	Tyr	Leu	Ser	Gln	Leu	Asn	Glu	Arg	Leu	Ser	Ala
				85					90					95	
Leu	Ala	Gly	Arg	Phe	Tyr	His	Glu	Pro	Ser	Asp	Asn	Leu	Arg	Leu	Val
			100					105					110		
Gly	Val	Thr	Gly	Thr	Asn	Gly	Lys	Thr	Thr	Thr	Thr	Gln	Leu	Leu	Ala
		115					120					125			
Gln	Trp	Ser	Gln	Leu	Leu	Gly	Glu	Ile	Ser	Ala	Val	Met	Gly	Thr	Val
		130				135						140			
Gly	Asn	Gly	Leu	Leu	Gly	Lys	Val	Ile	Pro	Thr	Glu	Asn	Thr	Thr	Gly
145					150					155					160
Ser	Ala	Val	Asp	Val	Gln	His	Glu	Leu	Ala	Gly	Leu	Val	Asp	Gln	Gly
			165						170					175	
Ala	Thr	Phe	Cys	Ala	Met	Glu	Val	Ser	Ser	His	Gly	Leu	Val	Gln	His
			180					185					190		
Arg	Val	Ala	Ala	Leu	Lys	Phe	Ala	Ala	Ser	Val	Phe	Thr	Asn	Leu	Ser
		195					200					205			
Arg	Asp	His	Leu	Asp	Tyr	His	Gly	Asp	Met	Glu	His	Tyr	Glu	Ala	Ala
		210				215					220				
Lys	Trp	Leu	Leu	Tyr	Ser	Glu	His	His	Cys	Gly	Gln	Ala	Ile	Ile	Asn
225					230					235					240
Ala	Asp	Asp	Glu	Val	Gly	Arg	Arg	Trp	Leu	Ala	Lys	Leu	Pro	Asp	Ala
			245						250					255	
Val	Ala	Val	Ser	Met	Glu	Asp	His	Ile	Asn	Pro	Asn	Cys	His	Gly	Arg
			260				265					270			
Trp	Leu	Lys	Ala	Thr	Glu	Val	Asn	Tyr	His	Asp	Ser	Gly	Ala	Thr	Ile
		275				280						285			
Arg	Phe	Ser	Ser	Ser	Trp	Gly	Asp	Gly	Glu	Ile	Glu	Ser	His	Leu	Met
		290				295					300				
Gly	Ala	Phe	Asn	Val	Ser	Asn	Leu	Leu	Leu	Ala	Leu	Ala	Thr	Leu	Leu
305					310					315					320
Ala	Leu	Gly	Tyr	Pro	Leu	Ala	Asp	Leu	Leu	Lys	Thr	Ala	Ala	Arg	Leu
			325						330					335	
Gln	Pro	Val	Cys	Gly	Arg	Met	Glu	Val	Phe	Thr	Ala	Pro	Gly	Lys	Pro
			340					345					350		
Thr	Val	Val	Val	Asp	Tyr	Ala	His	Thr	Pro	Asp	Ala	Leu	Glu	Lys	Ala
		355					360					365			
Leu	Gln	Ala	Ala	Arg	Leu	His	Cys	Ala	Gly	Lys	Leu	Trp	Cys	Val	Phe
		370				375					380				
Gly	Cys	Gly	Gly	Asp	Arg	Asp	Lys	Gly	Lys	Arg	Pro	Leu	Met	Gly	Ala
385					390					395					400
Ile	Ala	Glu	Glu	Phe	Ala	Asp	Val	Ala	Val	Val	Thr	Asp	Asp	Asn	Pro
				405					410					415	
Arg	Thr	Glu	Glu	Pro	Arg	Ala	Ile	Ile	Asn	Asp	Ile	Leu	Ala	Gly	Met
		420					425					430			
Leu	Asp	Ala	Gly	His	Ala	Lys	Val	Met	Glu	Gly	Arg	Ala	Glu	Ala	Val
		435					440					445			

Thr Cys Ala Val Met Gln Ala Lys Glu Asn Asp Val Val Leu Val Ala
 450 455 460
 Gly Lys Gly His Glu Asp Tyr Gln Ile Val Gly Asn Gln Arg Leu Asp
 465 470 475 480
 Tyr Ser Asp Arg Val Thr Val Ala Arg Leu Leu Gly Val Ile Ala
 485 490 495

<210> 450
 <211> 452
 <212> PRT
 <213> Escherichia coli

<400> 450
 Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1 5 10 15
 Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
 20 25 30
 Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
 35 40 45
 Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
 50 55 60
 Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65 70 75 80
 Lys Asp Thr Arg Leu Ala Phe Gly Glu Leu Ala Ala Trp Val Arg Gln
 85 90 95
 Gln Val Pro Ala Arg Val Val Ala Leu Thr Gly Ser Ser Gly Lys Thr
 100 105 110
 Ser Val Lys Glu Met Thr Ala Ala Ile Leu Ser Gln Cys Gly Asn Thr
 115 120 125
 Leu Tyr Thr Ala Gly Asn Leu Asn Asn Asp Ile Gly Val Pro Met Thr
 130 135 140
 Leu Leu Arg Leu Thr Pro Glu Tyr Asp Tyr Ala Val Ile Glu Leu Gly
 145 150 155 160
 Ala Asn His Gln Gly Glu Ile Ala Trp Thr Val Ser Leu Thr Arg Pro
 165 170 175
 Glu Ala Ala Leu Val Asn Asn Leu Ala Ala Ala His Leu Glu Gly Phe
 180 185 190
 Gly Ser Leu Ala Gly Val Ala Lys Ala Lys Gly Glu Ile Phe Ser Gly
 195 200 205
 Leu Pro Glu Asn Gly Ile Ala Ile Met Asn Ala Asp Asn Asn Asp Trp
 210 215 220
 Leu Asn Trp Gln Ser Val Ile Gly Ser Arg Lys Val Trp Arg Phe Ser
 225 230 235 240
 Pro Asn Ala Ala Asn Ser Asp Phe Thr Ala Thr Asn Ile His Val Thr
 245 250 255
 Ser His Gly Thr Glu Phe Thr Leu Gln Thr Pro Thr Gly Ser Val Asp
 260 265 270
 Val Leu Leu Pro Leu Pro Gly Arg His Asn Ile Ala Asn Ala Leu Ala
 275 280 285
 Ala Ala Ala Leu Ser Met Ser Val Gly Ala Thr Leu Asp Ala Ile Lys
 290 295 300
 Ala Gly Leu Ala Asn Leu Lys Ala Val Pro Gly Arg Leu Phe Pro Ile
 305 310 315 320
 Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn
 325 330 335
 Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly

340 345 350
 Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser
 355 360 365
 Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile
 370 375 380
 Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala
 385 390 395 400
 Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg
 405 410 415
 Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys
 420 425 430
 Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu
 435 440 445
 Asn Gly Thr Cys
 450

<210> 451
 <211> 360
 <212> PRT
 <213> Escherichia coli

<400> 451
 Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe
 1 5 10 15
 Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr
 20 25 30
 Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu
 35 40 45
 Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser
 50 55 60
 His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu
 65 70 75 80
 Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro
 85 90 95
 Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly
 100 105 110
 Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu
 115 120 125
 Ile Ala Arg Trp Lys Tyr Phe Trp Met Ser Val Ile Ala Leu Gly Val
 130 135 140
 Ala Phe Ala Leu Tyr Leu Ala Gly Lys Asp Thr Pro Ala Thr Gln Leu
 145 150 155 160
 Val Val Pro Phe Phe Lys Asp Val Met Pro Gln Leu Gly Leu Phe Tyr
 165 170 175
 Ile Leu Leu Ala Tyr Phe Val Ile Val Gly Thr Gly Asn Ala Val Asn
 180 185 190
 Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Phe Val
 195 200 205
 Ala Gly Gly Phe Ala Leu Val Ala Trp Ala Thr Gly Asn Met Asn Phe
 210 215 220
 Ala Ser Tyr Leu His Ile Pro Tyr Leu Arg His Ala Gly Glu Leu Val
 225 230 235 240
 Ile Val Cys Thr Ala Ile Val Gly Ala Gly Leu Gly Phe Leu Trp Phe
 245 250 255
 Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
 260 265 270

Leu Gly Gly Ala Leu Gly Ile Ile Ala Val Leu Leu Arg Gln Glu Phe
 275 280 285
 Leu Leu Val Ile Met Gly Gly Val Phe Val Val Glu Thr Leu Ser Val
 290 295 300
 Ile Leu Gln Val Gly Ser Phe Lys Leu Arg Gly Gln Arg Ile Phe Arg
 305 310 315 320
 Met Ala Pro Ile His His Tyr Glu Leu Lys Gly Trp Pro Glu Pro
 325 330 335
 Arg Val Ile Val Arg Phe Trp Ile Ile Ser Leu Met Leu Val Leu Ile
 340 345 350
 Gly Leu Ala Thr Leu Lys Val Arg
 355 360

<210> 452

<211> 438

<212> PRT

<213> Escherichia coli

<400> 452

Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu
 1 5 10 15
 Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro
 20 25 30
 Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
 35 40 45
 Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
 50 55 60
 Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
 65 70 75 80
 Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile
 85 90 95
 Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly
 100 105 110
 Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys
 115 120 125
 Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala
 130 135 140
 Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser
 145 150 155 160
 Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr
 165 170 175
 Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu
 180 185 190
 Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val
 195 200 205
 Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala
 210 215 220
 Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu
 225 230 235 240
 Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val
 245 250 255
 Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn
 260 265 270
 Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala
 275 280 285
 Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe

290		295		300
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys				
305		310		320
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val				
	325		330	335
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp				
	340		345	350
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr				
	355	360		365
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val				
370		375		380
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro				
385		390		400
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser				
	405		410	415
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg				
	420		425	430
Leu Ala Lys Glu Leu Gly				
435				

<210> 453
 <211> 414
 <212> PRT
 <213> Escherichia coli

<400> 453
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe
1 5 10 15
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
20 25 30
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu
35 40 45
Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr
50 55 60
Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe
65 70 75 80
Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala
85 90 95
Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala
100 105 110
Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val
115 120 125
Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu
130 135 140
Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile
145 150 155 160
Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg
165 170 175
Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu
180 185 190
Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr
195 200 205
Leu Ala Met Leu Phe Leu Ala Gly Ala Lys Leu Trp Gln Phe Ile Ala
210 215 220
Ile Ile Gly Met Gly Ile Ser Ala Val Val Leu Leu Ile Leu Ala Glu
225 230 235 240

210	215	220
Ser Val Glu Gln Ala Tyr Ala Glu Ala Gly Gln Pro Gln His Lys Val		
225	230	235
Thr Glu Phe Ile Asp Asp Met Ala Ala Ala Tyr Ala Trp Ala Asp Val		240
	245	250
Val Val Cys Arg Ser Gly Ala Leu Thr Val Ser Glu Ile Ala Ala Ala		255
	260	265
Gly Leu Pro Ala Leu Phe Val Pro Phe Gln His Lys Asp Arg Gln Gln		270
	275	280
Tyr Trp Asn Ala Leu Pro Leu Glu Lys Ala Gly Ala Ala Lys Ile Ile		285
	290	295
Glu Gln Pro Gln Leu Ser Val Asp Ala Val Ala Asn Thr Leu Ala Gly		300
305	310	315
Trp Ser Arg Glu Thr Leu Leu Thr Met Ala Glu Arg Ala Arg Ala Ala		320
	325	330
Ser Ile Pro Asp Ala Thr Glu Arg Val Ala Asn Glu Val Ser Arg Val		335
	340	345
Ala Arg Ala		350
355		

<210> 455
 <211> 491
 <212> PRT
 <213> Escherichia coli

<400> 455
Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met
1 5 10 15
Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met
20 25 30
Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly
35 40 45
Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly
50 55 60
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser
65 70 75 80
Val Val Val Val Ser Ser Ala Ile Ser Ala Asp Asn Pro Glu Ile Val
85 90 95
Ala Ala His Glu Ala Arg Ile Pro Val Ile Arg Arg Ala Glu Met Leu
100 105 110
Ala Glu Leu Met Arg Phe Arg His Gly Ile Ala Ile Ala Gly Thr His
115 120 125
Gly Lys Thr Thr Thr Thr Ala Met Val Ser Ser Ile Tyr Ala Glu Ala
130 135 140
Gly Leu Asp Pro Thr Phe Val Asn Gly Gly Leu Val Lys Ala Ala Gly
145 150 155 160
Val His Ala Arg Leu Gly His Gly Arg Tyr Leu Ile Ala Glu Ala Asp
165 170 175
Glu Ser Asp Ala Ser Phe Leu His Leu Gln Pro Met Val Ala Ile Val
180 185 190
Thr Asn Ile Glu Ala Asp His Met Asp Thr Tyr Gln Gly Asp Phe Glu
195 200 205
Asn Leu Lys Gln Thr Phe Ile Asn Phe Leu His Asn Leu Pro Phe Tyr
210 215 220
Gly Arg Ala Val Met Cys Val Asp Asp Pro Val Ile Arg Glu Leu Leu
225 230 235 240

<210> 458
 <211> 475
 <212> PRT
 <213> Escherichia coli

<400> 458

Met	Asn	Thr	Ala	Leu	Ala	Gln	Gln	Ile	Ala	Asn	Glu	Gly	Gly	Val	Glu
1				5					10					15	
Ala	Trp	Met	Ile	Ala	Gln	Gln	His	Lys	Ser	Leu	Leu	Arg	Phe	Leu	Thr
		20						25					30		
Cys	Gly	Ser	Val	Asp	Asp	Gly	Lys	Ser	Thr	Leu	Ile	Gly	Arg	Leu	Leu
		35					40					45			
His	Asp	Thr	Arg	Gln	Ile	Tyr	Glu	Asp	Gln	Leu	Ser	Ser	Leu	His	Asn
	50					55					60				
Asp	Ser	Lys	Arg	His	Gly	Thr	Gln	Gly	Glu	Lys	Leu	Asp	Leu	Ala	Leu
65					70					75					80
Leu	Val	Asp	Gly	Leu	Gln	Ala	Glu	Arg	Glu	Gln	Gly	Ile	Thr	Ile	Asp
			85						90					95	
Val	Ala	Tyr	Arg	Tyr	Phe	Ser	Thr	Glu	Lys	Arg	Lys	Phe	Ile	Ile	Ala
		100						105					110		
Asp	Thr	Pro	Gly	His	Glu	Gln	Tyr	Thr	Arg	Asn	Met	Ala	Thr	Gly	Ala
	115						120					125			
Ser	Thr	Cys	Glu	Leu	Ala	Ile	Leu	Leu	Ile	Asp	Ala	Arg	Lys	Gly	Val
	130					135					140				
Leu	Asp	Gln	Thr	Arg	Arg	His	Ser	Phe	Ile	Ser	Thr	Leu	Leu	Gly	Ile
145					150					155					160
Lys	His	Leu	Val	Val	Ala	Ile	Asn	Lys	Met	Asp	Leu	Val	Asp	Tyr	Ser
			165						170					175	
Glu	Glu	Thr	Phe	Thr	Arg	Ile	Arg	Glu	Asp	Tyr	Leu	Thr	Phe	Ala	Gly
			180					185					190		
Gln	Leu	Pro	Gly	Asn	Leu	Asp	Ile	Arg	Phe	Val	Pro	Leu	Ser	Ala	Leu
	195					200						205			
Glu	Gly	Asp	Asn	Val	Ala	Ser	Gln	Ser	Glu	Ser	Met	Pro	Trp	Tyr	Ser
	210				215						220				
Gly	Pro	Thr	Leu	Leu	Glu	Val	Leu	Glu	Thr	Val	Glu	Ile	Gln	Arg	Val
225					230					235					240
Val	Asp	Ala	Gln	Pro	Met	Arg	Phe	Pro	Val	Gln	Tyr	Val	Asn	Arg	Pro
			245						250					255	
Asn	Leu	Asp	Phe	Arg	Gly	Tyr	Ala	Gly	Thr	Leu	Ala	Ser	Gly	Arg	Val
		260						265					270		
Glu	Val	Gly	Gln	Arg	Val	Lys	Val	Leu	Pro	Ser	Gly	Val	Glu	Ser	Asn
	275					280						285			
Val	Ala	Arg	Ile	Val	Thr	Phe	Asp	Gly	Asp	Arg	Glu	Glu	Ala	Phe	Ala
	290					295					300				
Gly	Glu	Ala	Ile	Thr	Leu	Val	Leu	Thr	Asp	Glu	Ile	Asp	Ile	Ser	Arg
305					310					315					320
Gly	Asp	Leu	Leu	Leu	Ala	Ala	Asp	Glu	Ala	Leu	Pro	Ala	Val	Gln	Ser
			325						330					335	
Ala	Ser	Val	Asp	Val	Val	Trp	Met	Ala	Glu	Gln	Pro	Leu	Ser	Pro	Gly
			340					345					350		
Gln	Ser	Tyr	Asp	Ile	Lys	Ile	Ala	Gly	Lys	Lys	Thr	Arg	Ala	Arg	Val
	355					360						365			
Asp	Gly	Ile	Arg	Tyr	Gln	Val	Asp	Ile	Asn	Asn	Leu	Thr	Gln	Arg	Glu
	370					375					380				
Val	Glu	Asn	Leu	Pro	Leu	Asn	Gly	Ile	Gly	Leu	Val	Asp	Leu	Thr	Phe

385		390		395		400									
Asp	Glu	Pro	Leu	Val	Leu	Asp	Arg	Tyr	Gln	Gln	Asn	Pro	Val	Thr	Gly
		405		410		415									
Gly	Leu	Ile	Phe	Ile	Asp	Arg	Leu	Ser	Asn	Val	Thr	Val	Gly	Ala	Gly
		420		425		430									
Met	Val	His	Glu	Pro	Val	Ser	Gln	Ala	Thr	Ala	Ala	Pro	Ser	Glu	Phe
		435		440		445									
Ser	Ala	Phe	Glu	Leu	Glu	Leu	Asn	Ala	Leu	Val	Arg	Arg	His	Phe	Pro
		450		455		460									
His	Trp	Gly	Ala	Arg	Asp	Leu	Leu	Gly	Asp	Lys					
465				470		475									

<210> 459
 <211> 127
 <212> PRT
 <213> Escherichia coli

<400> 459
Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
1 5 10 15
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
20 25 30
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
35 40 45
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
50 55 60
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65 70 75 80
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
85 90 95
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
100 105 110
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu
115 120 125

<210> 460
 <211> 329
 <212> PRT
 <213> Escherichia coli

<400> 460
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
1 5 10 15
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
20 25 30
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu
35 40 45
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val
50 55 60
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu
65 70 75 80
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp
85 90 95
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala
100 105 110

				165						170					175
Lys	Met	Glu	Gly	Thr	Phe	Lys	Arg	Lys	Pro	Glu	Arg	Ser	Asp	Leu	Ser
			180					185					190		
Ala	Asp	Ile	Asn	Glu	His	Leu	Ile	Val	Glu	Leu	Tyr	Ser	Lys		
		195					200					205			

<210> 462
 <211> 129
 <212> PRT
 <213> Escherichia coli

<400> 462

Met	Ala	Lys	Ala	Pro	Ile	Arg	Ala	Arg	Lys	Arg	Val	Arg	Lys	Gln	Val
1				5					10					15	
Ser	Asp	Gly	Val	Ala	His	Ile	His	Ala	Ser	Phe	Asn	Asn	Thr	Ile	Val
			20					25					30		
Thr	Ile	Thr	Asp	Arg	Gln	Gly	Asn	Ala	Leu	Gly	Trp	Ala	Thr	Ala	Gly
		35					40					45			
Gly	Ser	Gly	Phe	Arg	Gly	Ser	Arg	Lys	Ser	Thr	Pro	Phe	Ala	Ala	Gln
		50				55					60				
Val	Ala	Ala	Glu	Arg	Cys	Ala	Asp	Ala	Val	Lys	Glu	Tyr	Gly	Ile	Lys
65					70					75					80
Asn	Leu	Glu	Val	Met	Val	Lys	Gly	Pro	Gly	Pro	Gly	Arg	Glu	Ser	Thr
				85					90					95	
Ile	Arg	Ala	Leu	Asn	Ala	Ala	Gly	Phe	Arg	Ile	Thr	Asn	Ile	Thr	Asp
			100					105						110	
Val	Thr	Pro	Ile	Pro	His	Asn	Gly	Cys	Arg	Pro	Pro	Lys	Lys	Arg	Arg
			115				120						125		

Val

<210> 463
 <211> 118
 <212> PRT
 <213> Escherichia coli

<400> 463

Met	Ala	Arg	Ile	Ala	Gly	Ile	Asn	Ile	Pro	Asp	His	Lys	His	Ala	Val
1				5					10					15	
Ile	Ala	Leu	Thr	Ser	Ile	Tyr	Gly	Val	Gly	Lys	Thr	Arg	Ser	Lys	Ala
			20					25					30		
Ile	Leu	Ala	Ala	Ala	Gly	Ile	Ala	Glu	Asp	Val	Lys	Ile	Ser	Glu	Leu
		35					40					45			
Ser	Glu	Gly	Gln	Ile	Asp	Thr	Leu	Arg	Asp	Glu	Val	Ala	Lys	Phe	Val
		50				55					60				
Val	Glu	Gly	Asp	Leu	Arg	Arg	Glu	Ile	Ser	Met	Ser	Ile	Lys	Arg	Leu
65					70					75					80
Met	Asp	Leu	Gly	Cys	Tyr	Arg	Gly	Leu	Arg	His	Arg	Arg	Gly	Leu	Pro
				85					90					95	
Val	Arg	Gly	Gln	Arg	Thr	Lys	Thr	Asn	Ala	Arg	Thr	Arg	Lys	Gly	Pro
			100					105						110	

Arg Lys Pro Ile Lys Lys
 115

				405					410				415				
Ala	Gly	Met	Phe	Ile	Met	Leu	Ser	Leu	Tyr	Lys	Leu	Thr	Asp	Ala	Arg		
			420					425					430				
Val	Glu	Ala	Ile	Ser	Arg	Gln	Leu	Ile	Lys	His	Arg	Ala	Ala	Gln	Gly		
		435				440						445					
Glu	Ala	Val	Pro	Asp	Ala	Ala	Thr	Ala	Ala	Ser	His						
	450					455					460						

<210> 465
 <211> 536
 <212> PRT
 <213> Escherichia coli

<400> 465

Met	Glu	Ile	Thr	Asn	Pro	Ile	Leu	Thr	Gly	Phe	Asn	Pro	Asp	Pro	Ser		
1				5					10					15			
Leu	Cys	Arg	Gln	Gly	Glu	Asp	Tyr	Tyr	Ile	Ala	Thr	Ser	Thr	Phe	Glu		
			20					25					30				
Trp	Phe	Pro	Gly	Val	Arg	Ile	Tyr	His	Ser	Arg	Asp	Leu	Lys	Asn	Trp		
		35				40						45					
Ser	Leu	Val	Ser	Thr	Pro	Leu	Asp	Arg	Val	Ser	Met	Leu	Asp	Met	Lys		
	50					55					60						
Gly	Asn	Pro	Asp	Ser	Gly	Gly	Ile	Trp	Ala	Pro	Cys	Leu	Ser	Tyr	Ala		
65				70					75					80			
Asp	Gly	Lys	Phe	Trp	Leu	Leu	Tyr	Thr	Asp	Val	Lys	Ile	Val	Asp	Ser		
			85					90						95			
Pro	Trp	Lys	Asn	Gly	Arg	Asn	Phe	Leu	Val	Thr	Ala	Pro	Ser	Ile	Glu		
			100					105						110			
Gly	Pro	Trp	Ser	Glu	Pro	Ile	Pro	Met	Gly	Asn	Gly	Gly	Phe	Asp	Pro		
		115				120						125					
Ser	Leu	Phe	His	Asp	Asp	Asp	Gly	Arg	Lys	Tyr	Tyr	Ile	Tyr	Arg	Pro		
	130				135					140							
Trp	Gly	Pro	Arg	His	His	Ser	Asn	Pro	His	Asn	Thr	Ile	Val	Leu	Gln		
145				150					155					160			
Ala	Phe	Asp	Pro	Gln	Thr	Gly	Thr	Leu	Ser	Pro	Glu	Arg	Lys	Thr	Leu		
			165					170						175			
Phe	Thr	Gly	Thr	Pro	Leu	Cys	Tyr	Thr	Glu	Gly	Ala	His	Leu	Tyr	Arg		
		180				185						190					
His	Ala	Gly	Trp	Tyr	Tyr	Leu	Met	Ala	Ala	Glu	Gly	Gly	Thr	Ser	Tyr		
	195				200							205					
Glu	His	Ala	Val	Val	Val	Leu	Arg	Ser	Lys	Asn	Ile	Asp	Gly	Pro	Tyr		
	210				215						220						
Glu	Leu	His	Pro	Asp	Val	Thr	Met	Met	Thr	Ser	Trp	His	Leu	Pro	Glu		
225				230					235					240			
Asn	Pro	Leu	Gln	Lys	Ser	Gly	His	Gly	Ser	Leu	Leu	Gln	Thr	His	Thr		
			245					250						255			
Gly	Glu	Trp	Tyr	Met	Ala	Tyr	Leu	Thr	Ser	Arg	Pro	Leu	Arg	Leu	Pro		
		260				265						270					
Gly	Val	Pro	Leu	Leu	Ala	Ser	Gly	Gly	Arg	Gly	Tyr	Cys	Pro	Leu	Gly		
	275				280						285						
Arg	Glu	Thr	Gly	Ile	Ala	Arg	Ile	Glu	Trp	Arg	Asp	Gly	Trp	Pro	Tyr		
	290			295						300							
Val	Glu	Gly	Gly	Lys	His	Ala	Gln	Leu	Thr	Val	Lys	Gly	Pro	Gln	Val		
305				310				315						320			
Ala	Glu	Gln	Pro	Ala	Ala	Val	Pro	Gly	Asn	Trp	Arg	Asp	Asp	Phe	Asp		
			325					330						335			

Ile	Asn	Thr	Pro	Ile	Lys	Val	Ser	Ala	Glu	Pro	Asn	Gly	Ala	Arg	Leu
				245					250					255	
Val	Glu	Val	His	Gln	Pro	Leu	Ser	Glu	Lys	Ile	Asp	Asp	Asp	Pro	Gln
			260					265					270		
Leu	Leu	Pro	Ile	Thr	Leu	Asn	Ser	Ala	Met	Gln	Ser	Phe	Lys	Asp	Ala
		275					280					285			
Ala	Gln	Thr	Asp	Ala	Glu	Val	Met	Gln	His	Val	Met	Asp	Val	Arg	Ser
	290					295					300				
Gly	Met	Pro	Val	Asp	Val	Arg	Arg	His	Gln	Val	Ser	Pro	Gln	Thr	Leu
305					310					315					320

<210> 468
 <211> 494
 <212> PRT
 <213> Escherichia coli

<400> 468

Met	Val	Ala	Ile	His	Leu	Leu	Pro	Val	Ser	Tyr	Asn	Ser	Ala	Thr	Ser
1				5					10					15	
Thr	Val	Asn	Ile	Ser	Ala	Arg	Ile	Ile	Pro	Leu	Leu	Ile	Ile	His	Gln
		20						25					30		
Arg	Tyr	Lys	Ile	Pro	Met	Pro	Lys	Val	Gln	Ala	Asp	Gly	Leu	Pro	Leu
		35				40						45			
Pro	Gln	Arg	Tyr	Gly	Ala	Ile	Leu	Thr	Ile	Val	Ile	Gly	Ile	Ser	Met
	50					55					60				
Ala	Val	Leu	Asp	Gly	Ala	Ile	Ala	Asn	Val	Ala	Leu	Pro	Thr	Ile	Ala
65					70				75						80
Thr	Asp	Leu	His	Ala	Thr	Pro	Ala	Ser	Ser	Ile	Trp	Val	Val	Asn	Ala
			85					90						95	
Tyr	Gln	Ile	Ala	Ile	Val	Ile	Ser	Leu	Leu	Ser	Phe	Ser	Phe	Leu	Gly
		100						105					110		
Asp	Met	Phe	Gly	Tyr	Arg	Arg	Ile	Tyr	Lys	Cys	Gly	Leu	Val	Val	Phe
		115					120					125			
Leu	Leu	Ser	Ser	Leu	Phe	Cys	Ala	Leu	Ser	Asp	Ser	Leu	Gln	Met	Leu
	130					135					140				
Thr	Leu	Ala	Arg	Val	Ile	Gln	Gly	Phe	Gly	Gly	Ala	Ala	Leu	Met	Ser
145					150					155					160
Val	Asn	Thr	Ala	Leu	Ile	Arg	Leu	Ile	Tyr	Pro	Gln	Arg	Phe	Leu	Gly
			165						170					175	
Arg	Gly	Met	Gly	Ile	Asn	Ser	Phe	Ile	Val	Ala	Val	Ser	Ser	Ala	Ala
		180					185						190		
Gly	Pro	Thr	Ile	Ala	Ala	Ala	Ile	Leu	Ser	Ile	Ala	Ser	Trp	Lys	Trp
	195						200					205			
Leu	Phe	Leu	Ile	Asn	Val	Pro	Leu	Gly	Ile	Ile	Ala	Leu	Leu	Leu	Ala
	210					215					220				
Met	Arg	Phe	Leu	Pro	Pro	Asn	Gly	Ser	Arg	Ala	Ser	Lys	Pro	Arg	Phe
225					230					235					240
Asp	Leu	Pro	Ser	Ala	Val	Met	Asn	Ala	Leu	Thr	Phe	Gly	Leu	Leu	Ile
			245						250				255		
Thr	Ala	Leu	Ser	Gly	Phe	Ala	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Ile	Ala
		260						265					270		
Ala	Glu	Leu	Val	Val	Met	Val	Val	Val	Gly	Ile	Phe	Phe	Ile	Arg	Arg
	275							280				285			
Gln	Leu	Ser	Leu	Pro	Val	Pro	Leu	Leu	Pro	Val	Asp	Leu	Leu	Arg	Ile
	290					295					300				
Pro	Leu	Phe	Ser	Leu	Ser	Ile	Cys	Thr	Ser	Val	Cys	Ser	Phe	Cys	Ala

305					310					315				320
Gln	Met	Leu	Ala	Met	Val	Ser	Leu	Pro	Phe	Tyr	Leu	Gln	Thr	Val
				325					330					335
Gly	Arg	Ser	Glu	Val	Glu	Thr	Gly	Leu	Leu	Leu	Thr	Pro	Trp	Pro
			340					345					350	
Ala	Thr	Met	Val	Met	Ala	Pro	Leu	Ala	Gly	Tyr	Leu	Ile	Glu	Arg
		355					360					365		Val
His	Ala	Gly	Leu	Leu	Gly	Ala	Leu	Gly	Leu	Phe	Ile	Met	Ala	Ala
	370					375					380			Gly
Leu	Phe	Ser	Leu	Val	Leu	Leu	Pro	Ala	Ser	Pro	Ala	Asp	Ile	Asn
	385				390					395				400
Ile	Trp	Pro	Met	Ile	Leu	Cys	Gly	Ala	Gly	Phe	Gly	Leu	Phe	Gln
			405						410					415
Pro	Asn	Asn	His	Thr	Ile	Ile	Thr	Ser	Ala	Pro	Arg	Glu	Arg	Ser
			420					425					430	Gly
Gly	Ala	Ser	Gly	Met	Leu	Gly	Thr	Ala	Arg	Leu	Leu	Gly	Gln	Ser
		435					440					445		Ser
Gly	Ala	Ala	Leu	Val	Ala	Leu	Met	Leu	Asn	Gln	Phe	Gly	Asp	Asn
	450					455					460			Gly
Thr	His	Val	Ser	Leu	Met	Ala	Ala	Ala	Ile	Leu	Ala	Val	Ile	Ala
	465				470					475				480
Cys	Val	Ser	Gly	Leu	Arg	Ile	Thr	Gln	Pro	Arg	Ser	Arg	Ala	
				485					490					

<210> 469
 <211> 477
 <212> PRT
 <213> Escherichia coli

<400> 469														
Met	Lys	Val	Thr	Leu	Pro	Glu	Phe	Glu	Arg	Ala	Gly	Val	Met	Val
1				5				10				15		
Gly	Asp	Val	Met	Leu	Asp	Arg	Tyr	Trp	Tyr	Gly	Pro	Thr	Ser	Arg
		20					25					30		Ile
Ser	Pro	Glu	Ala	Pro	Val	Pro	Val	Val	Lys	Val	Asn	Thr	Ile	Glu
		35				40					45			Glu
Arg	Pro	Gly	Gly	Ala	Ala	Asn	Val	Ala	Met	Asn	Ile	Ala	Ser	Leu
	50				55					60				Gly
Ala	Asn	Ala	Arg	Leu	Val	Gly	Leu	Thr	Gly	Ile	Asp	Asp	Ala	Ala
	65				70				75					80
Ala	Leu	Ser	Lys	Ser	Leu	Ala	Asp	Val	Asn	Val	Lys	Cys	Asp	Phe
			85					90					95	Val
Ser	Val	Pro	Thr	His	Pro	Thr	Ile	Thr	Lys	Leu	Arg	Val	Leu	Ser
		100						105				110		Arg
Asn	Gln	Gln	Leu	Ile	Arg	Leu	Asp	Phe	Glu	Glu	Gly	Phe	Glu	Gly
	115					120					125			Val
Asp	Pro	Gln	Pro	Leu	His	Glu	Arg	Ile	Asn	Gln	Ala	Leu	Ser	Ser
	130					135					140			Ile
Gly	Ala	Leu	Val	Leu	Ser	Asp	Tyr	Ala	Lys	Gly	Ala	Leu	Ala	Ser
	145				150					155				Val
Gln	Gln	Met	Ile	Gln	Leu	Ala	Arg	Lys	Ala	Gly	Val	Pro	Val	Leu
			165					170					175	Ile
Asp	Pro	Lys	Gly	Thr	Asp	Phe	Glu	Arg	Tyr	Arg	Gly	Ala	Thr	Leu
		180					185					190		Leu
Thr	Pro	Asn	Leu	Ser	Glu	Phe	Glu	Ala	Val	Val	Gly	Lys	Cys	Lys
		195					200					205		Thr

<210> 472
 <211> 207
 <212> PRT
 <213> Escherichia coli

<400> 472

Met	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Leu	Lys	Asp	Ala	Gly	Ile	Ser	Leu
1			5						10					15	
Thr	Asp	His	Gln	Lys	Asn	Gln	Leu	Ile	Ala	Tyr	Val	Asn	Met	Leu	His
			20					25					30		
Lys	Trp	Asn	Lys	Ala	Tyr	Asn	Leu	Thr	Ser	Val	Arg	Asp	Pro	Asn	Glu
		35					40					45			
Met	Leu	Val	Arg	His	Ile	Leu	Asp	Ser	Ile	Val	Val	Ala	Pro	Tyr	Leu
	50					55					60				
Gln	Gly	Glu	Arg	Phe	Ile	Asp	Val	Gly	Thr	Gly	Pro	Gly	Leu	Pro	Gly
65					70				75						80
Ile	Pro	Leu	Ser	Ile	Val	Arg	Pro	Glu	Ala	His	Phe	Thr	Leu	Leu	Asp
			85						90					95	
Ser	Leu	Gly	Lys	Arg	Val	Arg	Phe	Leu	Arg	Gln	Val	Gln	His	Glu	Leu
			100					105					110		
Lys	Leu	Glu	Asn	Ile	Glu	Pro	Val	Gln	Ser	Arg	Val	Glu	Glu	Phe	Pro
		115					120					125			
Ser	Glu	Pro	Pro	Phe	Asp	Gly	Val	Ile	Ser	Arg	Ala	Phe	Ala	Ser	Leu
	130					135					140				
Asn	Asp	Met	Val	Ser	Trp	Cys	His	His	Leu	Pro	Gly	Glu	Gln	Gly	Arg
145					150					155					160
Phe	Tyr	Ala	Leu	Lys	Gly	Gln	Met	Pro	Glu	Asp	Glu	Ile	Ala	Leu	Leu
				165					170						175
Pro	Glu	Glu	Tyr	Gln	Val	Glu	Ser	Val	Val	Lys	Leu	Gln	Val	Pro	Ala
			180					185					190		
Leu	Asp	Gly	Glu	Arg	His	Leu	Val	Val	Ile	Lys	Ala	Asn	Lys	Ile	
		195					200						205		

<210> 473
 <211> 629
 <212> PRT
 <213> Escherichia coli

<400> 473

Met	Phe	Tyr	Pro	Asp	Pro	Phe	Asp	Val	Ile	Ile	Ile	Gly	Gly	Gly	His
1				5					10					15	
Ala	Gly	Thr	Glu	Ala	Ala	Met	Ala	Ala	Ala	Arg	Met	Gly	Gln	Gln	Thr
			20					25					30		
Leu	Leu	Leu	Thr	His	Asn	Ile	Asp	Thr	Leu	Gly	Gln	Met	Ser	Cys	Asn
		35					40					45			
Pro	Ala	Ile	Gly	Gly	Ile	Gly	Lys	Gly	His	Leu	Val	Lys	Glu	Val	Asp
	50					55					60				
Ala	Leu	Gly	Gly	Leu	Met	Ala	Lys	Ala	Ile	Asp	Gln	Ala	Gly	Ile	Gln
65					70				75						80
Phe	Arg	Ile	Leu	Asn	Ala	Ser	Lys	Gly	Pro	Ala	Val	Arg	Ala	Thr	Arg
				85					90					95	
Ala	Gln	Ala	Asp	Arg	Val	Leu	Tyr	Arg	Gln	Ala	Val	Arg	Thr	Ala	Leu
			100					105					110		
Glu	Asn	Gln	Pro	Asn	Leu	Met	Ile	Phe	Gln	Gln	Ala	Val	Glu	Asp	Leu
		115					120					125			
Ile	Val	Glu	Asn	Asp	Arg	Val	Val	Gly	Ala	Val	Thr	Gln	Met	Gly	Leu

His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr
 595 600 605
 Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met
 610 615 620
 Leu Arg Arg Ser Ala
 625

<210> 474
 <211> 147
 <212> PRT
 <213> Escherichia coli

<400> 474
 Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu
 1 5 10 15
 Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr
 20 25 30
 Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly
 35 40 45
 Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp
 50 55 60
 Asn Leu Ser Pro Phe Tyr Glu Ala Leu Gln Glu Gln Lys Pro Asp Leu
 65 70 75 80
 Ser Ala Val Arg Phe Gly Ala Ile Gly Ile Gly Ser Arg Glu Tyr Asp
 85 90 95
 Thr Phe Cys Gly Ala Ile Asp Lys Leu Glu Ala Glu Leu Lys Asn Ser
 100 105 110
 Gly Ala Lys Gln Thr Gly Glu Thr Leu Lys Ile Asn Ile Leu Asp His
 115 120 125
 Asp Ile Pro Glu Asp Pro Ala Glu Glu Trp Leu Gly Ser Trp Val Asn
 130 135 140
 Leu Leu Lys
 145

<210> 475
 <211> 151
 <212> PRT
 <213> Escherichia coli

<400> 475
 Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
 1 5 10 15
 Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
 20 25 30
 Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser
 35 40 45
 Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
 50 55 60
 Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
 65 70 75 80
 Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
 85 90 95
 Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
 100 105 110
 Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser

	115		120		125
Gln	Ala Val Ile Arg Ser	Gly Glu Cys Ser Pro	Tyr Ala Asn Ile Ile		
	130	135	140		
Leu	Cys Ala Gly Val Thr	Phe			
145		150			

<210> 476
 <211> 501
 <212> PRT
 <213> Escherichia coli

<400> 476

Met	Glu	Ala	Leu	Leu	Gln	Leu	Lys	Gly	Ile	Asp	Lys	Ala	Phe	Pro	Gly
1				5					10					15	
Val	Lys	Ala	Leu	Ser	Gly	Ala	Ala	Leu	Asn	Val	Tyr	Pro	Gly	Arg	Val
			20					25					30		
Met	Ala	Leu	Val	Gly	Glu	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Met	Met	Lys
		35				40						45			
Val	Leu	Thr	Gly	Ile	Tyr	Thr	Arg	Asp	Ala	Gly	Thr	Leu	Leu	Trp	Leu
	50					55					60				
Gly	Lys	Glu	Thr	Thr	Phe	Thr	Gly	Pro	Lys	Ser	Ser	Gln	Glu	Ala	Gly
65					70					75					80
Ile	Gly	Ile	Ile	His	Gln	Glu	Leu	Asn	Leu	Ile	Pro	Gln	Leu	Thr	Ile
				85				90						95	
Ala	Glu	Asn	Ile	Phe	Leu	Gly	Arg	Glu	Phe	Val	Asn	Arg	Phe	Gly	Lys
			100					105					110		
Ile	Asp	Trp	Lys	Thr	Met	Tyr	Ala	Glu	Ala	Asp	Lys	Leu	Leu	Ala	Lys
		115				120						125			
Leu	Asn	Leu	Arg	Phe	Lys	Ser	Asp	Lys	Leu	Val	Gly	Asp	Leu	Ser	Ile
	130					135					140				
Gly	Asp	Gln	Gln	Met	Val	Glu	Ile	Ala	Lys	Val	Leu	Ser	Phe	Glu	Ser
145					150					155					160
Lys	Val	Ile	Ile	Met	Asp	Glu	Pro	Thr	Asp	Ala	Leu	Thr	Asp	Thr	Glu
				165					170					175	
Thr	Glu	Ser	Leu	Phe	Arg	Val	Ile	Arg	Glu	Leu	Lys	Ser	Gln	Gly	Arg
			180					185					190		
Gly	Ile	Val	Tyr	Ile	Ser	His	Arg	Met	Lys	Glu	Ile	Phe	Glu	Ile	Cys
		195				200						205			
Asp	Asp	Val	Thr	Val	Phe	Arg	Asp	Gly	Gln	Phe	Ile	Ala	Glu	Arg	Glu
	210					215					220				
Val	Ala	Ser	Leu	Thr	Glu	Asp	Ser	Leu	Ile	Glu	Met	Met	Val	Gly	Arg
225					230					235					240
Lys	Leu	Glu	Asp	Gln	Tyr	Pro	His	Leu	Asp	Lys	Ala	Pro	Gly	Asp	Ile
			245						250					255	
Arg	Leu	Lys	Val	Asp	Asn	Leu	Cys	Gly	Pro	Gly	Val	Asn	Asp	Val	Ser
			260					265					270		
Phe	Thr	Leu	Arg	Lys	Gly	Glu	Ile	Leu	Gly	Val	Ser	Gly	Leu	Met	Gly
		275					280					285			
Ala	Gly	Arg	Thr	Glu	Leu	Met	Lys	Val	Leu	Tyr	Gly	Ala	Leu	Pro	Arg
	290					295					300				
Thr	Ser	Gly	Tyr	Val	Thr	Leu	Asp	Gly	His	Glu	Val	Val	Thr	Arg	Ser
305					310					315					320
Pro	Gln	Asp	Gly	Leu	Ala	Asn	Gly	Ile	Val	Tyr	Ile	Ser	Glu	Asp	Arg
			325						330					335	
Lys	Arg	Asp	Gly	Leu	Val	Leu	Gly	Met	Ser	Val	Lys	Glu	Asn	Met	Ser
			340					345					350		

Leu Thr Ala Leu Arg Tyr Phe Ser Arg Ala Gly Gly Ser Leu Lys His
 355 360 365
 Ala Asp Glu Gln Gln Ala Val Ser Asp Phe Ile Arg Leu Phe Asn Val
 370 375 380
 Lys Thr Pro Ser Met Glu Gln Ala Ile Gly Leu Leu Ser Gly Gly Asn
 385 390 395 400
 Gln Gln Lys Val Ala Ile Ala Arg Gly Leu Met Thr Arg Pro Lys Val
 405 410 415
 Leu Ile Leu Asp Glu Pro Thr Arg Gly Val Asp Val Gly Ala Lys Lys
 420 425 430
 Glu Ile Tyr Gln Leu Ile Asn Gln Phe Lys Ala Asp Gly Leu Ser Ile
 435 440 445
 Ile Leu Val Ser Ser Glu Met Pro Glu Val Leu Gly Met Ser Asp Arg
 450 455 460
 Ile Ile Val Met His Glu Gly His Leu Ser Gly Glu Phe Thr Arg Glu
 465 470 475 480
 Gln Ala Thr Gln Glu Val Leu Met Ala Ala Ala Val Gly Lys Leu Asn
 485 490 495
 Arg Val Asn Gln Glu
 500

<210> 477
 <211> 321
 <212> PRT
 <213> Escherichia coli

<400> 477
 Met Thr Thr Gln Thr Val Ser Gly Arg Arg Tyr Phe Thr Lys Ala Trp
 1 5 10 15
 Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile
 20 25 30
 Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn
 35 40 45
 Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr
 50 55 60
 Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu
 65 70 75 80
 Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn
 85 90 95
 Ala Leu Val Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly
 100 105 110
 Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile
 115 120 125
 Ala Thr Leu Val Met Met Leu Leu Arg Gly Val Thr Met Val Tyr
 130 135 140
 Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu
 145 150 155 160
 Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val
 165 170 175
 Trp Ile Met Gly Ile Val Phe Leu Ala Ala Trp Tyr Met Leu His His
 180 185 190
 Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala
 195 200 205
 Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr
 210 215 220
 Ser Leu Cys Gly Leu Leu Ala Ser Leu Ala Gly Ile Ile Glu Val Ala

225		230		235		240									
Arg	Leu	Ser	Ser	Ala	Gln	Pro	Thr	Ala	Gly	Thr	Gly	Tyr	Glu	Leu	Asp
				245					250					255	
Ala	Ile	Ala	Ala	Val	Val	Leu	Gly	Gly	Thr	Ser	Leu	Ala	Gly	Gly	Lys
			260					265					270		
Gly	Arg	Ile	Val	Gly	Thr	Leu	Ile	Gly	Ala	Leu	Ile	Leu	Gly	Phe	Leu
		275					280					285			
Asn	Asn	Gly	Leu	Asn	Leu	Leu	Gly	Val	Ser	Ser	Tyr	Tyr	Gln	Met	Ile
	290						295				300				
Val	Lys	Ala	Val	Val	Ile	Leu	Leu	Ala	Val	Leu	Val	Asp	Asn	Lys	Lys
305					310					315				320	
Gln															

<210> 478
 <211> 296
 <212> PRT
 <213> Escherichia coli

<400> 478
Met Asn Met Lys Lys Leu Ala Thr Leu Val Ser Ala Val Ala Leu Ser
1 5 10 15
Ala Thr Val Ser Ala Asn Ala Met Ala Lys Asp Thr Ile Ala Leu Val
20 25 30
Val Ser Thr Leu Asn Asn Pro Phe Val Ser Leu Lys Asp Gly Ala
35 40 45
Gln Lys Glu Ala Asp Lys Leu Gly Tyr Asn Leu Val Val Leu Asp Ser
50 55 60
Gln Asn Asn Pro Ala Lys Glu Leu Ala Asn Val Gln Asp Leu Thr Val
65 70 75 80
Arg Gly Thr Lys Ile Leu Leu Ile Asn Pro Thr Asp Ser Asp Ala Val
85 90 95
Gly Asn Ala Val Lys Met Ala Asn Gln Ala Asn Ile Pro Val Ile Thr
100 105 110
Leu Asp Arg Gln Ala Thr Lys Gly Glu Val Val Ser His Ile Ala Ser
115 120 125
Asp Asn Val Leu Gly Gly Lys Ile Ala Gly Asp Tyr Ile Ala Lys Lys
130 135 140
Ala Gly Glu Gly Ala Lys Val Ile Glu Leu Gln Gly Ile Ala Gly Thr
145 150 155 160
Ser Ala Ala Arg Glu Arg Gly Glu Gly Phe Gln Gln Ala Val Ala Ala
165 170 175
His Lys Phe Asn Val Leu Ala Ser Gln Pro Ala Asp Phe Asp Arg Ile
180 185 190
Lys Gly Leu Asn Val Met Gln Asn Leu Leu Thr Ala His Pro Asp Val
195 200 205
Gln Ala Val Phe Ala Gln Asn Asp Glu Met Ala Leu Gly Ala Leu Arg
210 215 220
Ala Leu Gln Thr Ala Gly Lys Ser Asp Val Met Val Val Gly Phe Asp
225 230 235 240
Gly Thr Pro Asp Gly Glu Lys Ala Val Asn Asp Gly Lys Leu Ala Ala
245 250 255
Thr Ile Ala Gln Leu Pro Asp Gln Ile Gly Ala Lys Gly Val Glu Thr
260 265 270
Ala Asp Lys Val Leu Lys Gly Glu Lys Val Gln Ala Lys Tyr Pro Val
275 280 285

Asp Leu Lys Leu Val Val Lys Gln
290 295

<210> 479
<211> 309
<212> PRT
<213> Escherichia coli

<400> 479

Met Gln Asn Ala Gly Ser Leu Val Val Leu Gly Ser Ile Asn Ala Asp
1 5 10 15
His Ile Leu Asn Leu Gln Ser Phe Pro Thr Pro Gly Glu Thr Val Thr
20 25 30
Gly Asn His Tyr Gln Val Ala Phe Gly Gly Lys Gly Ala Asn Gln Ala
35 40 45
Val Ala Ala Gly Arg Ser Gly Ala Asn Ile Ala Phe Ile Ala Cys Thr
50 55 60
Gly Asp Asp Ser Ile Gly Glu Ser Val Arg Gln Gln Leu Ala Thr Asp
65 70 75 80
Asn Ile Asp Ile Thr Pro Val Ser Val Ile Lys Gly Glu Ser Thr Gly
85 90 95
Val Ala Leu Ile Phe Val Asn Gly Glu Gly Glu Asn Val Ile Gly Ile
100 105 110
His Ala Gly Ala Asn Ala Ala Leu Ser Pro Ala Leu Val Glu Ala Gln
115 120 125
Arg Glu Arg Ile Ala Asn Ala Ser Ala Leu Leu Met Gln Leu Glu Ser
130 135 140
Pro Leu Glu Ser Val Met Ala Ala Ala Lys Ile Ala His Gln Asn Lys
145 150 155 160
Thr Ile Val Ala Leu Asn Pro Ala Pro Ala Arg Glu Leu Pro Asp Glu
165 170 175
Leu Leu Ala Leu Val Asp Ile Ile Thr Pro Asn Glu Thr Glu Ala Glu
180 185 190
Lys Leu Thr Gly Ile Arg Val Glu Asn Asp Glu Asp Ala Ala Lys Ala
195 200 205
Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
210 215 220
Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
225 230 235 240
Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
245 250 255
Phe Asn Gly Ala Leu Ile Thr Ala Leu Glu Glu Lys Pro Leu Pro
260 265 270
Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ile Ala Val Thr Arg
275 280 285
Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe
290 295 300
Leu Asp Arg Gln Arg
305

<210> 480
<211> 52
<212> DNA
<213> Artificial Sequence

